

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2003, 05:28:22 ; Search time 1928 Seconds

(Without alignments)
6378.664 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 506
Sequence: 1 aaagagactatgctcgttc.....aaaaaaaaaaaaaaaaaaaaa 506

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vr1:*
28: gb_gss11:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	494.4	97.7	633	14	CB164987 KS0600583
2	486	96.0	530	12	BM062133 KS01038H0
3	459	90.7	527	12	BM064680 KS01070A0
4	443.2	87.6	648	14	CB185066 KS04236T7

5	440.8	87.1	506	14	CB164889	CB164889 KS050143T
6	421	83.2	496	14	CB164824	CB164824 KS050003T
7	378	74.7	540	12	BM063527	BM063527 KS01056D1
8	376.4	74.4	580	12	BM065064	BM065064 KS01074E1
9	372.2	73.6	720	14	CB185076	CB185076 KS04192T7
10	364	71.9	545	14	CB185076	CB185076 KS12056G0
11	363.8	71.9	448	12	CB185076	CB185076 KS12056G0
12	363.6	71.9	535	12	BM063616	BM063616 KS01057E0
13	360	71.1	571	12	BM062737	BM062737 KS01046F0
14	356.8	70.5	537	14	CB151866	CB151866 KS09048E1
15	353.6	69.9	532	12	BM064540	BM064540 KS01068D0
16	353.6	69.9	522	12	BM064663	BM064663 KS01065H0
17	345.2	68.2	521	14	CB185076	CB185076 KS01057D1
18	343.2	67.8	416	14	CB185076	CB185076 KS12033G0
19	339.6	67.1	509	12	CB164909	CB164909 KS050169T
20	321.2	63.5	474	14	CB164909	CB164909 KS01029G1
21	302.8	59.8	481	12	CB151866	CB151866 KS01065D0
22	291.8	57.7	466	12	BM063884	BM063884 KS01060F0
23	286.2	56.6	447	14	CB185076	CB185076 KS12038D0
24	284.6	56.2	474	14	CB185076	CB185076 KS09023C0
25	261.6	51.7	672	12	BM064987	BM064987 KS01073F0
26	254.4	50.3	332	14	CB164858	CB164858 KS050090T
27	251.8	49.8	376	12	BM062401	BM062401 KS01042C0
28	249.4	49.3	574	12	BM067544	BM067544 KS08007B0
29	234	46.2	589	14	CB151866	CB151866 KS09062G0
30	231.6	45.8	536	12	BM063253	BM063253 KS01055C0
31	221	43.7	380	14	CB151462	CB151462 KS09025A0
32	218.4	43.2	573	14	CB151462	CB151462 KS12022C1
33	217.6	43.0	356	9	AA842822	AA842822 CFR3 FnuI
34	215	42.5	500	12	BM061668	BM061668 KS01033C1
35	205	40.5	318	14	CB151612	CB151612 KS09053G0
36	205	40.5	513	12	BM063138	BM063138 KS01052A0
37	204.6	40.4	521	12	BM064471	BM064471 KS01067E0
38	201	39.7	231	9	AF082706	AF082706 AF082706
39	199.6	39.4	358	9	AA840730	AA840730 CFR11 FnuI
40	197.4	39.0	437	14	CB151406	CB151406 KS09016E1
41	196	38.7	339	12	BM060748	BM060748 KS01018B0
42	195	38.5	283	9	AA840727	AA840727 CFR8 FnuI
43	192	37.9	643	12	BM064620	BM064620 KS01069C0
44	176.4	34.9	306	14	CB1517625	CB1517625 KS09086E0
45	168.6	33.3	504	12	BM062945	BM062945 KS01049C0

ALIGNMENTS

RESULT 1
LOCUS CB164987 633 bp mRNA linear EST 30-JAN-2003
DEFINITION KS06005832 KS06 Capsicum annuum cDNA, mRNA sequence.
ACCESSION CB164987
VERSION CB164987.1 GI:28151113
KEYWORDS
SOURCE
ORGANISM
Capsicum annuum
Capsicum annuum

REFERENCE
AUTHORS Lee,S.Y., Lee,M.Y., Lee,P.S., Choi,S.H. and Harn,C.H.
TITLE EST fragments generated by SSH of SIRO red- SIRO green/red
JOURNAL Unpublished
COMMENT Contact: Chee Hark Harn
Biotechnology center
NONG WO0 BIO CO., LTD.
537-17 Jeongdan, Gnam, Yeosu, Kyonggi 463-885, Republic of Korea
Tel: 82 31 883 7055
Fax: 82 31 884 7065
Email: chharn@nongwoobio.co.kr
Seq primer: 77
Location/Qualifiers
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/organism="Capsicum annuum"

FEATURES
source

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/mol_type="mRNA"
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/clone_lib="KS06"
/notes="Vector: pGEM-T easy; Site 1: EcoRI; SRO red - SRO
green/red suppression subtractive cDNA library of Hot
pepper. The subtraction was performed using the PCR-select
cDNA subtraction kit (Clontech, Palo Alto, CA) according
to the manufacturer's instructions. For a tester, cDNA
from HR-developing pepper leaves sampled after 3 days
transcription was synthesized using AMV reverse
transcriptase while, for a driver, cDNA from noninoculated
pepper leaves was synthesized. After the subtractive
hybridization, the subtracted cDNAs are selectively
amplified by using nested PCR primers to enrich
differentially expressed sequences."
BASE COUNT      212 a      103 c      118 g      197 t      3 others
ORIGIN
Query Match      97.7%; Score 494.4; DB 14; Length 633;
Best Local Similarity 98.6%; Pred. No. 4.9e-50;
Matches 498; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db  121  AAATGTTCTAGAGACCCCTGATGTCAAAAACCTGTAAGAGAGAAATATGAAAGT 253
Qy  121  AAATGTTCTAGAGACCCCTGATGTCAAAAACCTGTAAGAGAGAAATATGAAAGT 253
Db  121  AAATGTTCTAGAGACCCCTGATGTCAAAAACCTGTAAGAGAGAAATATGAAAGT 253
Qy  181  GGTCAATGTTTCAACAATCTTAAGCAAGTGTGATGCAAGAGATGTAATGCTAAACT 240
Db  254  GGTCATGTTTCAACAATCTTAAGCAAGTGTGATGCAAGAGATGTAATGCTAAACT 313
Qy  241  CTGCGACAAGAAATTCCTGCTGGAAGAGATTCCTCAAGCAGTAATTAAGTTGATTA 300
Db  314  CTGCGACAAGAAATTCCTGCTGGAAGAGATTCCTCAAGCAGTAATTAAGTTGATTA 373
Qy  301  GGATTTAGTGTCAACAATCTTAAGCAAGTGTGATGCAAGAGATGTAATGCTAAACT 360
Db  374  GGATTTAGTGTCAACAATCTTAAGCAAGTGTGATGCAAGAGATGTAATGCTAAACT 433
Qy  361  TGTGTAATCTTGGTGTATAGTATGAGCATTTGACACATTAATTAAGTTGTGACATCA 420
Db  434  TGTGTAATCTTGGTGTATAGTATGAGCATTTGACACATTAATTAAGTTGTGACATCA 493
Qy  421  ATCTTCATGATATCTTCTATTAAGTTGTGTTTATGAAAAGATCGTTTACGGTC 480
Db  494  ATCTTCATGATATCTTCTATTAAGTTGTGTTTATGAAAAGATCGTTTACGGTC 553
Qy  481  TAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 505
Db  554  TATATGTATATATATATATATATATATATATATATATATATATATATATATATAT 578

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Capsicum.
1 (bases 1 to 530)
Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S.,
Hur, C.-G. and Choi, D.
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen
Unpublished
Contact: Doil Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doil@mail.kribb.re.kr
High quality sequence stop: 530.
Location/Qualifiers
1..530
/organism="Capsicum annuum"
/mol_type="mRNA"
/db_xref="taxon:4072"
/tissue_type="leaf inoculated with Xanthomonas campestris
pv. glycines"
/dev_stage="8 weeks after germination"
/clone_lib="KS01"
/notes="Vector: pBluescript SK(-)"
BASE COUNT      176 a      76 c      99 g      179 t
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Best Local Similarity 98.8%; Pred. No. 5.4e-49;
Matches 500; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

1  AAAGAGACATGAGCTGCTGCTTACTTCAATGAGCATTTCTGCTGGCAATGACATC 60
Db  25  AAAGAGACATGAGCTGCTGCTTACTTCAATGAGCATTTCTGCTGGCAATGACATC 83
Qy  61  TTTGTTGCTTATGGGGTGCAGAGCAAGAAATTTGCTGTAAGAGCTCAAAAACCTGTT 120
Db  84  TTTGTTGCTTATGGGGTGCAGAGCAAGAAATTTGCTGTAAGAGCTCAAAAACCTGTT 143
Qy  121  AAATGTTCTAGAGACCCCTGATGTCAAAAACCTGTAAGAGAGAAATATGAAAGT 180
Db  144  AAATGTTCTAGAGACCCCTGATGTCAAAAACCTGTAAGAGAGAAATATGAAAGT 203
Qy  181  GGTCAATGTTTCAACAATCTTAAGCAAGTGTGATGCAAGAGATGTAATGCTAAACT 240
Db  204  GGTCATGTTTCAACAATCTTAAGCAAGTGTGATGCAAGAGATGTAATGCTAAACT 263
Qy  241  CTGCGACAAGAAATTCCTGCTGGAAGAGATTCCTCAAGCAGTAATTAAGTTGATTA 300
Db  264  CTGCGACAAGAAATTCCTGCTGGAAGAGATTCCTCAAGCAGTAATTAAGTTGATTA 323
Qy  301  GGATTTAGTGTCAACAATCTTAAGCAAGTGTGATGCAAGAGATGTAATGCTAAACT 360
Db  324  GGATTTAGTGTCAACAATCTTAAGCAAGTGTGATGCAAGAGATGTAATGCTAAACT 383
Qy  361  TGTGTAATCTTGGTGTATAGTATGAGCATTTGACACATTAATTAAGTTGTGACATCA 420
Db  384  TGTGTAATCTTGGTGTATAGTATGAGCATTTGACACATTAATTAAGTTGTGACATCA 443
Qy  421  ATCTTCATGATATCTTCTATTAAGTTGTGTTTATGAAAAGATCGTTTACGGTC 480
Db  444  ATCTTCATGATATCTTCTATTAAGTTGTGTTTATGAAAAGATCGTTTACGGTC 503
Qy  481  TAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 506
Db  504  TATATGTATATATATATATATATATATATATATATATATATATATATATATATAT 529

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BM064680
LOCUS BM064680 527 bp mRNA linear EST 11-SEP-2002
DEFINITION KS01070A06 KS01 Capsicum annuum cDNA, mRNA sequence.
ACCESSION BM064680
VERSION BM064680.1 GI:22784798
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 527)
Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pal, H.-S.,
Hur, C.-G. and Choi, D.
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen
JOURNAL Unpublished
COMMENT Contact: Doll Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doll@mail.kribb.re.kr
High quality sequence stop: 527.
Location/Qualifiers
1..527
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/mol_type="mRNA"
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/db_xref="taxon:4072"
/tissue_type="leaf inoculated with Xanthomonas campestris
pv. glycines"
/dev_stage="8 weeks after germination"
/clone_11b="KS01"
/note="Vector: pBluescript SK(-)"

BASE COUNT 175 a 74 c 100 g 178 t
ORIGIN
Query Match 90.7%; Score 459; DB 12; Length 527;
Best Local Similarity 96.7%; Pred. No. 8.7e-46;
Matches 492; Conservative 0; Mismatches 10; Indels 7; Gaps 2;

QY 1 AAAGAGACTATGAGCTGCTTCACTTACTTCAATGAGCATTTCTGCTTGGAGACACAC 60
DB 22 AAAGAGACTATGAGCTGCTTCACTTACTTCAATGAGCATTTCTGCTTGGAGACAC 81
QY 61 TTGTTGCTTATGGGGTGAAGGCAAGAAATTTGCTGTAAAGCTCACAACCTGTT 120
DB 82 TTGTTGCTTATGGGGTGAAGGCAAGAAATTTGCTGTAAAGCTCACAACCTGTT 141
QY 121 AAATGTTTCAAGTACCTCTATGTCAAAAACCTGTATGAGAAGAGAAATATGAAGAT 180
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DB 202 GGTCAATTTGTTCAATCTTAAGCAAGGCTTATGCAAGAAATATGCTAAACT 261
QY 241 CTGGCAACAGAAATGCTTGTGAAGAAGAGTTCTCAAGCAAGTAATTAAGTTGATAT 300
DB 262 CTGGCAACAGAAATGCTTGTGAAGAAGAGTTCTCAAGCAAGTAATTAAGTTGATAT 318
QY 301 GGAATTAAGTCAACAATAAT---TAAATAAGTGTGCTTTCTTAAAGGTAACCT 356
DB 319 GGAATTAAGTCAACAATAATTAATAAATAAGTGTGCTTTCTTAAAGGTAACCT 378
QY 357 ATAATGTTATTTCTTGTGTATAGTACCAATTTGACACATTAATTAAGTTGTGACAC 416
DB 379 ATAATGTTATTTCTTGTGTATAGTACCAATTTGACACATTAATTAAGTTGTGACAC 438
QY 417 ATCAATCCTTCAATGATCTTCTATTAAGTTGTGTTTAAAGAAAGATCGTTTAC 476

DB 439 ATCAATCCTTCAATGATCTTCTATTAAGTTGTGTTTAAAGAAAGATCGTTTAC 498
QY 477 GGTCTAAAAAAGGAG 505
DB 499 GGTCTATATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTT 527

RESULT 4
LOCUS CB185066 648 bp mRNA linear EST 03-FEB-2003
DEFINITION KS04236T70 KS04 Capsicum chinense cDNA, mRNA sequence.
ACCESSION CB185066
VERSION CB185066.1 GI:28197059
KEYWORDS EST.
SOURCE Capsicum chinense
ORGANISM Capsicum chinense
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 648)
Lee, S.J., Lee, M.Y., Choi, S.H., Her, N.H., Yang, S.G. and Hahn, C.H.
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
chinense) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen
JOURNAL Unpublished
COMMENT Contact: Chee Hark Harn
Biotechnology center
NONG WOONG BIO CO., LTD.
537-17 Jeongdan, Ganam, Yeosu, Kyonggi 469-885, Republic of Korea
Tel: 82 31 883 7055
Fax: 82 31 884 7065
Email: charn@nongwoobio.co.kr
Seq primer: T7.
Location/Qualifiers
1..648
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/db_xref="taxon:80379"
/sex="hermaphrodite"
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/dev_stage="7-8 weeks-old leaves"
/clone_11b="KS04"
/note="Vector: pGEM-T easy; Site 1: EcoRI; PMW-induced
suppression subtractive cDNA library of Hot pepper. The
subtraction was performed using the PCR-select cDNA
subtraction kit (Clontech, Palo Alto, CA) according to the
manufacturer's instructions. For a tester, cDNA from
HR-developing pepper leaves sampled after 3 days
inoculation was synthesized using AMV reverse
transcriptase while, for a driver, cDNA from noninoculated
pepper leaves was synthesized. After the subtractive
hybridization, the subtracted cDNAs are selectively
amplified by using nested PCR primers to enrich
differentially expressed sequences."

BASE COUNT 197 a 115 c 132 g 196 t 8 others
ORIGIN
Query Match 87.6%; Score 443.2; DB 14; Length 648;
Best Local Similarity 93.1%; Pred. No. 5.8e-44;
Matches 471; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 AAAGAGACTATGAGCTGCTTCACTTACTTCAATGAGCATTTCTGCTTGGAGACAC 60
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QY 61 TTGTTGCTTATGGGGTGAAGGCAAGAAATTTGCTGTAAAGCTCACAACCTGTT 120
DB 183 TTGTTGCTTATGGGGTGAAGGCAAGAAATTTGCTGTAAAGCTCACAACCTGTT 242
QY 121 AAATGTTTCAAGTACCTCTATGTCAAAAACCTGTATGAGAAGAGAAATATGAAGAT 180

Db 243 AATGTTCTAGTAGACCTCTATGTCAAAACTCTGTATGAGAGAGAAATATGAAAGAT 302
 Qy 181 GGCATTTGTTTCACATCTCTAAGCAGGCTTANGCAGAGAAATATGCTAAACT 240
 Db 303 GGCATTTGTTTCACATCTCTAAGCAGGCTTANGCAGAGAAATATGCTAAACT 362
 Qy 241 CTCGACACAGAAATGCTGCTTGAAGAGAGTTCTCAAGCAGTAATTAAGTTGATAT 300
 Db 363 CTCGACACAGAAATGCTGCTTGAAGAGAGTTCTCAAGCAGTAATTAAGTTGATAT 422
 Qy 301 GGAATTAAGTGCACAAATTAATTAAGTTGCTTCTTAAAGGTAATCTATA 360
 Db 423 GGAATTAAGTGCACAAATTAATTAAGTTGCTTCTTAAAGGTAATCTATA 482
 Qy 361 TGTGTAATCTGCTGTATAGTACCATTTGACATTAATTAAGTTGACACATCA 420
 Db 483 TGTGTAATCTGCTGTATAGTACCATTTGACATTAATTAAGTTGACACATCA 542
 Qy 421 ATCCTTCATGTAATCTCTTATAGTTGTGTGTTTATGAAAGAGATGCTTACGTC 480
 Db 543 ATCCTTCATGTAATCTCTTATAGTTGTGTGTTTATGAAAGAGATGCTTACGTC 601
 Qy 481 TAAAAAATTAATTAAGTTGCTTCTTAAAGGTAATCTATA 506
 Db 602 CTTTGTGTTGAAAAAATTAAGTTGCTTCTTAAAGGTAATCTATA 627

RESULT 5
 CBI64889 506 bp mRNA linear EST 30-JAN-2003
 LOCUS KS05014310 KS05 Capsicum annuum cDNA, mRNA sequence.
 DEFINITION CBI64889
 ACCESSION CBI64889.1 GI:28151015
 VERSION
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Capsicum.
 1 (bases 1 to 506)
 Lee, S.J., Lee, M.Y., Lee, P.S., Choi, S.H. and Harn, C.H.
 EST fragments generated by SSH of SIRO red- SBV red
 Unpublished
 Contact: Chee Hark Harn
 Biotechnology center
 NONG WOONG BIO CO., LTD.
 537-17 Jeongdan, Ganam, Yeosu, Kyonggi 469-885, Republic of Korea
 Tel: 82 31 883 7065
 Fax: 82 31 884 7065
 Email: chharn@nongwoong.co.kr
 Seq primer: T7.
 Location/Qualifiers

FEATURES

SOURCE

1..506
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 /tissue_type="fruit"
 /dev_stage="mature red"
 /note="Vector: pGEM-T easy; Site1: EcoRI; SIRO red - SBV
 red suppression subtractive cDNA library of hot pepper.
 The subtraction was performed using the PCR-select cDNA
 subtraction kit (Clontech, Palo Alto, CA) according to the
 manufacturer's instructions. For a tester, cDNA from
 HR-developing pepper leaves sampled after 3 days
 inoculation was synthesized using AMV reverse
 transcriptase while, for a driver, cDNA from noninoculated
 pepper leaves was synthesized. After the subtractive
 hybridization, the subtracted cDNAs are selectively
 amplified by using nested PCR primers to enrich
 differentially expressed sequences."

BASE COUNT 154 a 82 c 101 g 169 t
 ORIGIN

Query Match 87.1%; Score 440.8; DB 14; Length 506;
 Best Local Similarity 99.5%; Pred. No. 1,3e-43;
 Matches 442; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGAGACATGAGCTGTTCCATTTACTTACATGTCATTTCTGCTTGGCAATGACATC 60
 Db 63 AAGAGACATGAGCTGTTCCATTTACTTACATGTCATTTCTGCTTGGCAATGACATC 122
 Qy 61 TTTGTTGCTTAATGAGGTCGACGACGAGAAATTTGCTGTAAAGCTCAAAAATCTGTT 120
 Db 123 TTTGTTGCTTAATGAGGTCGACGACGAGAAATTTGCTGTAAAGCTCAAAAATCTGTT 182
 Qy 121 AATGTTCTAGTACCCCTCTATGTCAAAACTCTGTATGAGAGAGAAATATGAAAGT 180
 Db 183 AATGTTCTAGTACCCCTCTATGTCAAAACTCTGTATGAGAGAGAAATATGAAAGT 242
 Qy 181 GGCATTTGTTTACAAATCTTAAAGAGCTTATGCAATGAGATGTAAGTAAACT 240
 Db 243 GGCATTTGTTTACAAATCTTAAAGAGCTTATGCAATGAGATGTAAGTAAACT 302
 Qy 241 CTCGACACAGAAATGCTGCTTGAAGAGAGTTCTTCAAGCAGTAATTAAGTTGATAT 300
 Db 303 CTCGACACAGAAATGCTGCTTGAAGAGAGTTCTTCAAGCAGTAATTAAGTTGATAT 362
 Qy 301 GGAATTAAGTGCACAAATTAATTAAGTTGCTTCTTAAAGGTAATCTATA 360
 Db 363 GGAATTAAGTGCACAAATTAATTAAGTTGCTTCTTAAAGGTAATCTATA 422
 Qy 361 TGTGTAATCTGCTGTATAGTACCATTTGACATTAATTAAGTTGACACATCA 420
 Db 423 TGTGTAATCTGCTGTATAGTACCATTTGACATTAATTAAGTTGACACATCA 482
 Qy 421 ATCCTTCATGTAATCTCTTATAGTTGTGTGTTTATGAAAGAGATGCTTACGTC 480
 Db 483 ATCCTTCATGTAATCTCTTATAGTTGTGTGTTTATGAAAGAGATGCTTACGTC 601

RESULT 6
 CBI64824 496 bp mRNA linear EST 30-JAN-2003
 LOCUS KS05000310 KS05 Capsicum annuum cDNA, mRNA sequence.
 DEFINITION CBI64824
 ACCESSION CBI64824.1 GI:28150950
 VERSION
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Capsicum.
 1 (bases 1 to 496)
 Lee, S.J., Lee, M.Y., Lee, P.S., Choi, S.H. and Harn, C.H.
 EST fragments generated by SSH of SIRO red- SBV red
 Unpublished
 Contact: Chee Hark Harn
 Biotechnology center
 NONG WOONG BIO CO., LTD.
 537-17 Jeongdan, Ganam, Yeosu, Kyonggi 469-885, Republic of Korea
 Tel: 82 31 883 7065
 Fax: 82 31 884 7065
 Email: chharn@nongwoong.co.kr
 Seq primer: T7.
 Location/Qualifiers

FEATURES

SOURCE

1..496
 /organism="Capsicum annuum"
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 /db_xref="taxon:4072"
 /sex="hermaphrodite"
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 /dev_stage="mature red"

REFERENCE 1 (bases 1 to 580)
 AUTHORS Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G. and Choi, D.
 TITLE Generation of Expressed Sequence Tags from Hot Pepper (*Capiscum annuum* L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
 JOURNAL Unpublished
 COMMENT Contact: Doll Choi
 Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doilemail.kr@ibb.re.kr
 High quality sequence stop: 580.
 Location/Qualifiers
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 /organism="Capiscum annuum"
 /mol_type="mRNA"
 /cultivar="Bukang"
 /db_xref="taxon:4072"
 /tissue_type="leaf inoculated with *Xanthomonas campestris* pv. *glyciniae*"
 /dev_stage="8 weeks after germination"
 /clone_lib="KS01"
 /note="Vector: pBluescript SK(-)"
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 Best Local Similarity 87.5%; Pred. No. 5.3e-36;
 Matches 453; Conservative 0; Mismatches 46; Indels 19; Gaps 3;
 Oy 1 AAGAGCATGCGCTGCTCCATTACTTCATGCGATTCCTGCTGGCAATGACACGC 60
 Db AAGAGCATGCGCTGCTCCATTACTTCATGCGATTCCTGCTGGCAATGACACGC 87
 Oy 28 AAGAGCATGCGCTGCTCCATTACTTCATGCGATTCCTGCTGGCAATGACACGC 87
 Db 61 TTTGTTGCTTAAGGGGTCAAGGCAAGAAATTTGCTGTAAAGCTCACAAACCTGTT 120
 Oy 88 TTTGTTGCTTAAGGGGTCAAGGCAAGAAATTTGCTGTAAAGCTCACAAACCTGTT 147
 Db 121 AAATGTTCTAGTACCCCTCTATGTCACAAAACCTGTATGAGAGAGAAATGGAAGAT 180
 Oy 148 ATATGTTCTAGTACCCCTCTATGTCACAAAACCTGTATGAGAGAGAAATGGAAGAT 207
 Db 181 GGTCAATTTTTCACATCTTAAGCAAGTGTCTTAAGCATGAAGAGATGA----- 229
 Oy 208 GGTCAATTTTTCACATCTTAAGCAAGTGTCTTAAGCATGAAGAGATGA----- 267
 Db 230 -ATGCTAAACCTGCGACAGAAATTTGCTGTGAAGAGAGATTTCTTCAAGCAGATAT 288
 Oy 268 GAGTTTAAACCTGCGACAGAAATTTGCTGTGAAGAGAGATTTCTTCAAGCAGATAT 327
 Db 289 AAGTTGATTAAGATTTAGTGTCAACAAAATTAATTAAGTGTGCTTTCTTAAAG 348
 Oy 328 AAGTTGATTAAGATTTAGTGTCAACAAAATTAATTAAGTGTGCTTTCTTAAAG 387
 Db 349 GGTAACTTAATATGTTGATTTCTGTGTATGATGAGCATTTGACATTAATTAAGT 408
 Oy 388 GGTAACTTAATATGTTGATTTCTGTGTATGATGAGCATTTGACATTAATTAAGT 446
 Db 409 TGTGAACATCAATCTTTCATGATCTTCTATTAAGTTGTGCTTTTAAAGAAAGAA 468
 Oy 447 TGTGAACATCAATCTTTCATGATCTTCTATTAAGTTGTGCTTTTAAAGAAAGAA 500
 Db 469 TCGTTTACGCTCAAAAAAAAAAAAAAAAAAAAAA 506
 Oy 501 TCGTTTACGCTCAAAAAAAAAAAAAAAAAAAAAA 538

LOCUS CB185076 720 bp mRNA linear EST 03-FEB-2003
 DEFINITION KS04192770 KS04 Capiscum chinense cDNA, mRNA sequence.
 ACCESSION CB185076
 VERSION CB185076.1 GI:28197069
 KEYWORDS EST.
 SOURCE Capiscum chinense
 ORGANISM Capiscum chinense
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 720)
 AUTHORS Lee, S.-J., Lee, M.-Y., Choi, S.-H., Her, N.-H., Yang, S.-G. and Harn, C.-H.
 TITLE Generation of Expressed Sequence Tags from Hot pepper (*Capiscum chinense*) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
 JOURNAL Unpublished
 COMMENT Contact: Chee Hark Harn
 Biotechnology center
 NONG WO0 BIO CO., LTD.
 537-17 Jeongdan, Ganam, Yeosu, Kyonggi 463-885, Republic of Korea
 Tel: 82 31 883 7055
 Fax: 82 31 884 7065
 Email: chharn@nongwoobio.co.kr
 Seq primer: 17.
 Location/Qualifiers
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 /organism="Capiscum chinense"
 /mol_type="mRNA"
 /cultivar="PI257284"
 /db_xref="taxon:80379"
 /sex="hermaphrodite"
 /tissue_type="leaf"
 /dev_stage="7-8 weeks-old leaves"
 /clone_lib="KS04"
 /note="Vector: pGEM-T easy; Site 1: EcoRI; PMV-induced suppression subtractive cDNA library of Hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."
 BASE COUNT 203 a 114 c 133 g 218 t 52 others
 ORIGIN
 Query Match 73.6%; Score 372.2; DB 14; Length 720;
 Best Local Similarity 90.5%; Pred. No. 1.5e-35;
 Matches 431; Conservative 0; Mismatches 37; Indels 8; Gaps 4;
 Oy 1 AAGAGCATGCGCTGCTCCATTACTTCATGCGATTCCTGCTGGCAATGACACGC 60
 Db 191 AAGAGCATGCGCTGCTCCATTACTTCATGCGATTCCTGCTGGCAATGACACGC 250
 Oy 61 TTTGTTGCTTAAGGGGTCAAGGCAAGAAATTTGCTGTAAAGCTCACAAACCTGTT 120
 Db 251 TTTGTTGCTTAAGGGGTCAAGGCAAGAAATTTGCTGTAAAGCTCACAAACCTGTT 310
 Oy 121 AAATGTTCTAGTACCCCTCTATGTCACAAAACCTGTATGAGAGAGAAATGGAAGAT 180
 Db 311 AAATGTTCTAGTACCCCTCTATGTCACAAAACCTGTATGAGAGAGAAATGGAAGAT 370
 Oy 181 GGTCAATTTTTCACATCTTAAGCAAGTGTCTTAAGCATGAAGAGATGA----- 240
 Db 371 GGTCAATTTTTCACATCTTAAGCAAGTGTCTTAAGCATGAAGAGATGA----- 430
 Oy 241 CTCGAACGAATTTGCTGTGAAGAGAGATTTCTTCAAGCAGATATTAAGTTGATTA 299
 Db 431 CTCGAACGAATTTGCTGTGAAGAGAGATTTCTTCAAGCAGATATTAAGTTGATTA 490

Oy	30	TGGATTAGTCACACAATAATTAATGAAGTGCGCTTCTTTAAA--GGGTAACTTA	357
Dd	491	TGGATTTAGTCACACAATAATTAATGAAGTGCGCTTCTTTAAAAGGCGTA	550
Oy	358	TAATGTTGATTTCTTGCTGA-TAGAGCCATTGCACACTTAATTAAGTTGACAC	416
Dd	551	TAAAGTTGAATCTTNGAANFAGTGGCATTTGACACTTAATTAANGTTGNAC	610
Oy	417	ATCAAT----CCTCANTATCTCTTTAAGTTTGCTTTTAATGAAGA	468
Dd	611	AACATTAATCCCTNNATGTTCTTNTATNAAGTTTNGCGANNITCAATGAANA	666
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RESULT 10			
LOCUS CA525505			
DEFINITION KS1205607 KS12 Capsicum annuum cDNA, mRNA sequence.			
VERSION CA525505			
KEYWORDS GI:25039585			
SOURCE EST.			
ORGANISM Capsicum annuum			
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.			
AUTHORS Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-U., Goh,S.-H., Pai,H.-S., Hur,C.-G. and Choi,D.			
TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen Unpublished			
JOURNAL Contact: Dail Choi;			
COMMENT Genome Research Center and National Center for Genome Information Korea Research Institute of Bioscience and Biotechnology P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea Tel: 82-42-860-4340 Fax: 82-42-860-4309 Email: doil@mail.kribb.re.kr Plate: 056 row: G column: 07.			
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FEATURES			
Source Location/Qualifiers			
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/db_xref="taxon:4072"			
/clone_lib="KS12"			
BASE COUNT 182 a 84 c 106 g 173 t			
ORIGIN			
Query Match 71.9%; Score 364; DB 14; Length 545;			
Best Local Similarity 86.5%; Pred. No. 1.6e-34;			
Matches 443; Conservative 0; Mismatches 50; Indels 19; Gaps 3;			
Oy	1	AAAGAGCATAGGCGTGTTCATTACTTCATGSCATTTCTGCTTGCAATGACACG	60
Dd	41	AAAGTGCATAGGCGTGTTCATTACTTCATGSCATTTCTGCTTGCAATGACCTC	100
Oy	61	TTTGTGCTTAGGGGTGCAGCAAGAAATTTGCTGTAAAGACTCAAAACCTGTT	120
Dd	101	TTTGTGCCCATAGAGGTGCAGGTAAAGAAATTTGCTGTAAAGATGCTCAAGAGCTGT	160
Oy	121	AAATGTTCTAGAGCCCTATGTCAAACCTGTGTAGGAAAGGAAATATGAGAT	180
Dd	161	ATATGTTCTTAGACCCTATGTAAACAAATCTGTATCGAAGAGGAACATAGAGAT	220
Oy	181	GGTCAATTTGTTCACAATCCTTAAGCAAGTGCTTATGATGAAGAGATGA-----	229
Dd	221	GGTCATTTGTTCACAATCCTTAAGGAAGGCGATATGATGAAGATGATATGTGTTCA	280
Oy	230	-ATGCTAAACCTGCCACAGAAATTCGCTGTGAAGAAGAGTCTCAAGCAATAT	288
Dd	281	GAATTTAAACCTCTCCAGCAAAATTCGCTGTGTGAAGAAGAGTTTCTCAAGCAATAT	340

QY	289	AAAGTTGATTAAGATTAAGTGTACACAAATAATTAAGTGTGCTTTCTTAAG	348
Db	341	AACTTTGATTAAGATTAAGTGTACACAAATAATTAAGTGTGCTTTCTTAAG	400
QY	349	GGTAACATAAATGTTGTAATCTTGATGTATAGTAGGACATTGACACATTAAATTAAGT	408
Db	401	GGTAACATAAATGTTGTAATCTTGATGTATAGTAGGACATTGACACATTAAATTAAGT	459
QY	409	TGTGACACATCAATCTTCATGTATCTTCTTATTAAGTTGTGTGTTTATGAAAGAGA	468
Db	460	TGTGACACATCAATCTTCATGTATCAACTT-----TGTGTGCTTTTAATGAAAGGA	513
QY	469	TGCTTTACGCTTAAAAAAAAAAAAAAAAAAAAA	500
Db	514	TGCTTTACCATCAAAAAAAAAAAAAAAAAAAAAA	545
RESULT 11			
LOCUS	EM063616	448 bp	mRNA linear EST 11-SEP-2002
DEFINITION	KS01057E08 KS01 Capsicum annuum cDNA, mRNA sequence.		
ACCESSION	EM063616		
VERSION	EM063616.1	GI:22783734	
KEYWORDS	EST.		
SOURCE	Capsicum annuum		
ORGANISM	Capsicum annuum		
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.		
AUTHORS	1 (bases 1 to 448)		
LEADS	Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G. and Choi, D.		
DESCRIPTION	Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen		
JOURNAL	Unpublished		
COMMENT	Contact: Doil Choi Genome Research Center and National Center for Genome Information Korea Research Institute of Bioscience and Biotechnology P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea Tel: 82-42-860-4340 Fax: 82-42-860-4309 Email: doil@mail.krdb.re.kr High quality sequence stop: 448.		
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SOURCE	1..448		
	/organism="Capsicum annuum"		
	/mol_type="mRNA"		
	/cultivar="Bukang"		
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	/tissue_type="leaf inoculated with Xanthomonas campestris pv. glycines"		
	/dev_stage="8 weeks after germination"		
	/clone_lib="KS01"		
	/note="Vector: pBluescript SK(-)"		
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ORIGIN			
Query Match	71.9%: Score 363.8; DB 12; Length 448;		
Best Local Similarity	99.5%; Pied No. 2e-34; 2; Indels 0; Gaps 0		
Matches	365; Conservative 0; Mismatches 2; Indels 0; Gaps 0		
QY	1	AAAGAGACTAATGCTGCTGCTCAATTTACTTCATGACATTTCTGTCTTGCGATGACATC	60
Db	45	AAAGAGACTAATGCTGCTGCTCAATTTACTTCATGACATTTCTGTCTTGCGATGACATC	104
QY	61	TTTGTGCTTAATGAGGTGCAAGCAAGAAATTTGCTGAAGAGCTCAAAATCTGTT	120
Db	105	TTTGTGCTTAATGAGGTGCAAGCAAGAAATTTGCTGAAGAGCTCAAAATCTGTT	164
QY	121	AAATGTTCTAAGACCTCTTATGTCAAAAATCTGTATGAGAGAGAAATTAAGAT	180
Db	165	AAATGTTCTAAGACCTCTTATGTCAAAAATCTGTATGAGAGAGAAATTAAGAT	224

QY 181 GGTGATTGTTACAGATCCGATGAGCAAGTGTCTTATGTCATGAGAGATGTAATGCTAAACCT 240
 DB 225 GGTGATTGTTACAGATCCGATGAGCAAGTGTCTTATGTCATGAGAGATGTAATGCTAAACCT 284
 QY 241 CTCGCAACAGAAATGCTGCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 300
 DB 285 CTCGCAACAGAAATGCTGCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 344
 QY 301 GGATTTAGTGCACAAATAATTAATTAAGTGTCTTCTTAAAGGGTAATTAATA 360
 DB 345 GGATTTAGTGCACAAATAATTAATTAAGTGTCTTCTTAAAGGGTAATTAATA 404
 QY 361 TGTGTA 367
 DB 405 TGTGTA 411

RESULT 12
 LOCUS BM062737 535 bp mRNA linear EST 11-SEP-2002
 DEFINITION KS01046F09 KS01 Capsicum annum cDNA, mRNA sequence.
 ACCESSION BM062737
 VERSION BM062737.1 GI:22782855
 KEYWORDS EST.
 SOURCE Capsicum annum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 535)
 AUTHORS Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G., and Choi, D.
 TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
 JOURNAL Unpublished
 COMMENT Contact: Doil Choi
 Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doilemail.kr@kribb.re.kr
 High quality sequence stop: 535.
 Location/Qualifiers
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 /organism="Capsicum annum"
 /mol_type="mRNA"
 /cultivar="Bukang"
 /db_xref="taxon:4072"
 /tissue_type="leaf inoculated with Xanthomonas campestris pv. glycines"
 /dev_stage="8 weeks after germination"
 /clone_idb="KS01"
 /note="Vector: pBluescript SK(-)"
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 Query Match 71.9%; Score 363.6; DB 12 Length 535;
 Best Local Similarity 85.9%; Pred. No. 1.8e-34;
 Matches 445; Conservative 0; Mismatches 54; Indels 19; Gaps 3;

DB 144 ATATGTTCTAGTACCCGCTATGTAAACAAATCTGTATGCAAGAGAGAACTATGAGAT 203
 QY 181 GGTGATTGTTACAGATCCGATGAGCAAGTGTCTTATGTCATGAGAGATGTAATGCTAAACCT 229
 DB 204 GGTGATTGTTACAGATCCGATGAGCAAGTGTCTTATGTCATGAGAGATGTAATGCTAAACCT 263
 QY 230 -ATGCTAAACTCTGCAACAGAAATGCTGCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 288
 DB 264 GATGTTAAACCTCTGCAACAGAAATGCTGCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 323
 QY 289 AAGTTGATTATGATTAATTAAGTGTCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 348
 DB 324 AAGTTGATTATGATTAATTAAGTGTCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 383
 QY 349 GGTAACTTAATTAATTAAGTGTCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 408
 DB 384 GGTAACTTAATTAATTAAGTGTCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 442
 QY 409 TGTGACATCAATCTTCATGATTAATTAAGTGTCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 468
 DB 443 TGTGACATCAATCTTCATGATTAATTAAGTGTCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 496
 QY 469 TGTGTTACGCTTAAAAAATTAATTAAGTGTCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 506
 DB 497 TGTGTTACGCTTAAAAAATTAATTAAGTGTCTTGAAGAGAGTTCCTCAAGCAATTAATTAAGTTATAT 534

RESULT 13
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 DEFINITION KS09048E11 KS09 Capsicum annum cDNA, mRNA sequence.
 ACCESSION CAS15866
 VERSION CAS15866.1 GI:25016423
 KEYWORDS EST.
 SOURCE Capsicum annum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 571)
 AUTHORS Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G., and Choi, D.
 TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
 JOURNAL Unpublished
 COMMENT Contact: Doil Choi
 Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doilemail.kr@kribb.re.kr
 Plate: 048 row: E column: 11.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /clone_idb="KS09"
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 Best Local Similarity 88.1%; Pred. No. 4.7e-34;
 Matches 453; Conservative 0; Mismatches 45; Indels 16; Gaps 5;

Db 106 TTGTGCTAGGAGGCTCAAGTAAGAAATTTGCTGTAAAGTCCCAACACCTTTT 165
 Qy 121 AAATGTTCTAGTACCCCTCTATGTCAAAAACCTGTATGAGAGAGAAATATGAAAT 180
 Db 166 CTATGCTCTAATGACCTCAATGCAAGACACTGCT---TCCAGGGAATCTAAGAAAT 222
 Qy 181 GGTCTATGTTTCAATCTTAAGCAAGGCTTTATGATGAAGATGT-----AATGCT 234
 Db 223 GGTCTATGTTTCAATCTTAAGCAAGGCTTTATGATGAAGATGT-----AATGCT 282
 Qy 235 AAAACTCTGCAACAGAAATGCTGCTTGAAGAGAGTCTCAAGCAGTAATTAATTT 294
 Db 283 AAAACCTGCAAGCAAA-----TTCCTGAAGAGAGTCTCAAGCAGTAATTAATTT 338
 Qy 295 GATTATGATTTAGTCTCAACAAATTAATTAAGTGTCCCTTTCTTAAAGGTAAC 354
 Db 339 AATTATGATTTAGTCTCAACAAATTAATTAAGTGTCCCTTTCTTAAAGGTAAC 398
 Qy 355 TTATATGTTGATTTCTTGCTATAGTACCATTTGACATTAATTAAGTGTGAC 414
 Db 399 TTATAGGTTGTTCTTGCTATAGTACCATTTGACATTAATTAAGTGTGAC 457
 Qy 415 ACATCAATCTTATGCTCTCTATTAAGTGTGCTTT--TAAAGAAAGATGCT 472
 Db 458 ACATCAATCTTATGCTCTCTATTAAGTGTGCTTTCTTAAAGAAAGATGCT 517
 Qy 473 TTACGCTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 506
 Db 518 TTACGCTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 551

RESULT 14
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 LOCUS KS01068D09 KS01 Capsicum annuum cDNA, mRNA sequence.
 DEFINITION BM064540
 ACCESSION BM064540
 VERSION BM064540.1 GI:22784658
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
 1 (bases 1 to 537)
 Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pal, H.-S., Hur, C.-G. and Choi, D.
 Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
 Unpublished
 Contact: Doil Choi
 Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doilemail.kr@ibb.re.kr
 High quality sequence stop: 537.
 Location/Qualifiers
 1..537

FEATURES
 source
 /organism="Capsicum annuum"
 /mol_type="mRNA"
 /cultivar="Bukang"
 /db_xref="taxon:4072"
 /tissue_type="leaf inoculated with Xanthomonas campestris pv. glycines"
 /dev_stage="8 weeks after germination"
 /clone_lib="KS01"
 /note="Vector: pBluescript SK(-)"

BASE COUNT 176 a 83 c 97 g 181 t
 ORIGIN
 Query Match 70.5%; Score 356.8; DB 12; Length 537;

Best Local Similarity 87.7%; Pred. No. 1,2e-33;
 Matches 451; Conservative 0; Mismatches 47; Indels 16; Gaps 5;
 Qy 1 AAAGACATATGAGCTGCTTCACTTACTTCAATGATTTCTTCTTGGCAATGACACTC 60
 Db 30 AAGACATATGAGCTGCTTCACTTACTTCAATGATTTCTTCTTGGCAATGACACTC 89
 Qy 61 TTGTGCTTATGAGGCTGCAAGCAGGAAATTTGCTGTAAAGCTCACAAACCTGTT 120
 Db 90 TTGTGCTTATGAGGCTGCAAGCAGGAAATTTGCTGTAAAGCTCACAAACCTGTT 149
 Qy 121 AAATGTTCTAGTACCCCTCTATGTCAAAAACCTGTATGAGAGAGAAATATGAAAT 180
 Db 150 CTATGCTCTAATGACCTCAATGCAAGACACTGCT---TCCAGGGAATCTAAGAAAT 206
 Qy 181 GGTCTATGTTTCAATCTTAAGCAAGGCTTTATGATGAAGATGT-----AATGCT 234
 Db 207 GGTCTATGTTTCAATCTTAAGCAAGGCTTTATGATGAAGATGT-----AATGCT 266
 Qy 235 AAAACTCTGCAACAGAAATGCTGCTTGAAGAGAGTCTCAAGCAGTAATTAATTT 294
 Db 267 AAAACCTGCAAGCAAA-----TTCCTGAAGAGAGTCTCAAGCAGTAATTAATTT 322
 Qy 295 GATTATGATTTAGTCTCAACAAATTAATTAAGTGTCCCTTTCTTAAAGGTAAC 354
 Db 323 AATTATGATTTAGTCTCAACAAATTAATTAAGTGTCCCTTTCTTAAAGGTAAC 382
 Qy 355 TTATATGTTGATTTCTTGCTATAGTACCATTTGACATTAATTAAGTGTGAC 414
 Db 383 TTATAGGTTGTTCTTGCTATAGTACCATTTGACATTAATTAAGTGTGAC 441
 Qy 415 ACATCAATCTTATGCTCTCTATTAAGTGTGCTTT--TAAAGAAAGATGCT 472
 Db 442 ACATCAATCTTATGCTCTCTATTAAGTGTGCTTTCTTAAAGAAAGATGCT 501
 Qy 473 TTACGCTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 506
 Db 502 TTACGCTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 535

RESULT 15
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 LOCUS KS01069H01 KS01 Capsicum annuum cDNA, mRNA sequence.
 DEFINITION BM064663
 ACCESSION BM064663
 VERSION BM064663.1 GI:22784781
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
 1 (bases 1 to 522)
 Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pal, H.-S., Hur, C.-G. and Choi, D.
 Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
 Unpublished
 Contact: Doil Choi
 Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doilemail.kr@ibb.re.kr
 High quality sequence stop: 522.
 Location/Qualifiers
 1..522

FEATURES
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 /organism="Capsicum annuum"
 /mol_type="mRNA"
 /cultivar="Bukang"
 /db_xref="taxon:4072"

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C	22	43.2	8.5	6219	12	US-10-311-855-839
C	23	43	8.5	2505	9	US-09-729-674-198
C	24	43	8.5	10329	12	US-10-311-455-2096
C	25	43	8.5	16724	12	US-10-311-455-1064
C	26	43	8.5	16724	12	US-10-240-485-90
C	27	43	8.5	17421	12	US-10-240-453-56
C	28	43	8.5	17421	14	US-10-239-676-54
C	29	42.8	8.5	1787	11	US-09-974-979-115
C	30	42.8	8.5	1787	11	US-09-305-736-116
C	31	42.8	8.5	2254	13	US-10-114-893-211
C	32	42.6	8.4	638	9	US-09-764-869-351
C	33	42.6	8.4	638	11	US-10-091-504-351
C	34	42.6	8.4	726	14	US-09-764-891-8400
C	35	42.4	8.4	2270	14	US-10-042-894X-24
C	36	42.4	8.4	2814	10	US-09-880-107-3419
C	37	42.4	8.4	2814	10	US-09-967-768A-191
C	38	42.4	8.4	2814	14	US-10-223-085-335
C	39	42.4	8.4	2814	14	US-10-223-084-335
C	40	42.4	8.4	2814	14	US-10-223-088-335
C	41	42.4	8.4	2814	14	US-10-223-090-335
C	42	42.4	8.4	2814	14	US-10-223-087-335
C	43	42.4	8.4	2814	14	US-10-223-083-335
C	44	42.4	8.4	2814	14	US-10-223-089-335
C	45	42.4	8.4	4657	9	US-09-766-870-239

ALIGNMENTS

RESULT 1
US-09-777-347-1

Sequence 1, Application US/09777347

Patent No. US2001001497A1

GENERAL INFORMATION:

APPLICANT: McBride, Kevin E.
Stalker, David M.

TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Calgene, Inc.

STREET: 1920 Filch Street

CITY: Davis

STATE: CA

COUNTRY: USA

ZIP: 95616

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB

OPERATING SYSTEM: Macintosh 7.1

SOFTWARE: Microsoft Word 5.1 (a)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/777,347

FILING DATE: 05-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,087

FILING DATE: <Unknown>

APPLICATION NUMBER: USSN 07/554,195

FILING DATE: 17-JUL-90

APPLICATION NUMBER: USSN 07/382,518

FILING DATE: 19-JUL-89

ATTORNEY/AGENT INFORMATION:
NAME: Carl J. Schwedler

REGISTRATION NUMBER: 36,924

REFERENCE/DOCKET NUMBER: CGNE 91-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313

TELEFAX: (916) 753-1510

INFORMATION FOR SEQ ID NO: 1
 SEQUENCE CHARACTERISTICS:
 LENGTH: 564 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 1
 US-09-777-347-1

Query Match 18.5%; Score 93.8; DB 9; Length 564;
 Best Local Similarity 61.2%; Pred. No. 1e-12;
 Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;

QY 8 CTATGGCTGCTTCATTTTCTCATGGCAATTCCTGCTTGGCAATGACATCTTTGTTG 67
 DB 38 CCATGGCTGCTTCATTTTCTCATGGCAATTTTGGCTTGGCAATGATCTCTTTGTTA 97
 QY 68 CTATGGGGTGAAGGCAAGCAATTTGCG--TGTAAAGAGCTCACAAACCTTTAAT 124
 DB 98 CTTATAGAGTAGAGCTCCAGCAATTTGCAAGCAACCAAGCAACTTTCCAGGATTA 157
 QY 125 GTTCTAGTACCTCTATGTCAAAAACCTGTGTATGAGAGAGAAATATGAGATGTC 184
 DB 158 GTTTATGAGCTCATCATGTAGAAAATTTGTAT--CAAGAGAAATTTACTGTGGAC 214
 QY 185 ATTGTTCAATTCCTTAAGCAAGTCTTATGATGAGAGATGTAATGCTAAACCTCG 244
 DB 215 ATTGTGCAAACTCCAAAGAGAGTCTATGCACTAAGCATGTATTTGACAAATCT 274
 QY 245 CAACAGATTT-----GCTTCCTTG 263
 DB 275 CAAGTAAAGTTAAAGCACTTGGGTGAGAGCAAAAATCTAAGTAAAGTGTGCTTG 334
 QY 264 AAGAGAGTTCCTCAAGCAGTAAAT--TAAGTTGATTAAGGATTTAGT-- 311
 DB 335 AAGAAAGATTAAGTATGAGTAAATTAAGTATGAGTAAATAGATTTTGAAGTGTCA 394
 QY 312 --CACCAAAATTAATTAAGTGTGCTTTCTTAAGAGCTAATTATATGTTG--T 366
 DB 395 AAAAAACAAATTAATTAAGTGTGCTTTCTTAAGAGTGTGCTGTGATGTGTGTT 454
 QY 367 ATTCTTGCTATAGTATGACATTTGACATTTAATTAAGTGTGACATCAATCTT 426
 DB 455 AGATATGGCTATAGTATGACATTTGACATTTAA--TAAGTTGTGACATCATCTAATC 513
 QY 427 CATGTATCTTCTATTAAGTGTGTGTTTAAAGAAAGAGATCTTTAGCGTTAAA 485
 DB 514 C-----TTATGTATGTATGTTTAAATGAATAATGATGACATGATCTTTTAA 560

RESULT 2

US-09-777-347-2
 Sequence 2, Application US/0977347
 Patent No. US28010014977A1

GENERAL INFORMATION:

APPLICANT: Mcbride, Kevin E.
 TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calgene, Inc.
 STREET: 1920 Fifth Street
 CITY: Davis
 STATE: CA
 COUNTRY: USA
 ZIP: 95616
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.1
 SOFTWARE: Microsoft Word 5.1 (a)
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/777,347
 FILING DATE: 05-Feb-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,087
 FILING DATE: <Unknown>
 APPLICATION NUMBER: USSN 07/554,195
 FILING DATE: 17-JUL-90
 APPLICATION NUMBER: USSN 07/382,518
 FILING DATE: 19-JUL-89

ATTORNEY/AGENT INFORMATION:

NAME: Carl J. Schmedler
 REGISTRATION NUMBER: 36,924
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510

INFORMATION FOR SEQ ID NO: 2

LENGTH: 3528 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double

MOLECULE TYPE: genomic DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 2
 US-09-777-347-2

Query Match 12.4%; Score 62.6; DB 9; Length 3528;
 Best Local Similarity 64.8%; Pred. No. 6e-05;
 Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;

QY 262 TGAAGAGAGTTCCTCAAGCAGTAAATTAAGTTGATTATGATTTAGTGTACACAAAT 321
 DB 3165 TGATGAGTAAATTAATTAAGAGAGCTTAATAAGATTTGAGTGTCAAAAAACAAAT 3224
 QY 322 TAAATTAAGTGTGCTTTCTTAAGAGGCTTAATGTTATGTTATTC--TTGGTGT 378
 DB 3225 TAAATTAAGTGTGCTTTCTTAAGAGGCTTAATGTTATGTTATGTTATGTTATG 3284
 QY 379 TAGTATGATTTGACATTAATTAAGTGTGACACATCAATCTTCATGATATCTTCT 438
 DB 3285 TAGTATGATTTGACATTAATTAAGTGTGACACATCAATCTTCATGATATCTTCT 3332
 QY 439 ATTAGTTGTGTGTTTAAATGAAGAGATCGTTTACGCTTAAA 485
 DB 3333 -TTATGTATGTATGTTTAAATGAAGAGATCGATCAATCTTTTAA 3378

RESULT 3

US-10-078-090-28
 Sequence 28, Application US/10078090
 Publication No. US20030044815A1

GENERAL INFORMATION:

APPLICANT: Salceda, Susana
 APPLICANT: Macina, Roberto
 APPLICANT: Hu, Ping
 APPLICANT: Recipon, Heve
 APPLICANT: Karra, Kaipana
 APPLICANT: Cafferey, Robert
 APPLICANT: Sun, Yongming
 APPLICANT: Liu, Chenshua
 TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
 FILE REFERENCE: DEX-0312
 CURRENT APPLICATION NUMBER: US/10/078,090
 PRIOR FILING DATE: 2002-02-14
 PRIOR APPLICATION NUMBER: 60/268,999
 NUMBER OF SEQ ID NOS: 210
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 28
 LENGTH: 1210
 TYPE: DNA
 ORGANISM: Homo sapien

FEATURE:
NAME/KEY: misc.feature
LOCATION: (631)..(631)
OTHER INFORMATION: a, c, g or t
US-10-078-090-28

Query Match 10.0%; Score 50.4; DB 14; Length 1210;
Best Local Similarity 52.9%; Pred. No. 0.03;
Matches 108; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 303 ATTTAGTGTACACAAATTAATTAAGTGTGCTTTCTTAAGAGGTAATTAAG 362
DB ATGTCACTACACTGGAATTAATTAATTAATTAATTAATTAATTAATTAAT 460
QY 363 TTGTATCTGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 422
DB 461 TTGAATGTATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 520
QY 423 CCTCATGATCTCTATTAATTAATTAATTAATTAATTAATTAATTAATTA 482
DB 521 AGTCACTGATTTGCAATTAATTAATTAATTAATTAATTAATTAATTAAT 580
QY 483 AAAAAAAAAAAAAAAAAAAAAA 506
DB 581 AAAAAAAAAAAAAAAAAAAAAA 604

RESULT 4

US-10-311-455-602/c
Sequence 602, Application US/10311455
Publication No. US200301435606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311.455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 602
LENGTH: 7669
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US-10-311-455-602

Query Match 9.8%; Score 49.8; DB 12; Length 7669;
Best Local Similarity 58.4%; Pred. No. 0.094;
Matches 87; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 357 ATAAATGTTATCTTGTGTATAGTACCATTTGACACATTAATTAAGTGTGACAC 416
DB 435 ATAAATATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 376
QY 417 ATAAATCTCATGATCTCTATTAATTAAGTGTGTGTTTAATGAAGATCGTTAC 476
DB 375 TTAATAATTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 316
QY 477 GGTCTAAAAAAAAAAAAAAAAAAAAA 505
DB 315 AATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 287

RESULT 5

US-10-066-543-593/c
Sequence 593, Application US/10066543
Publication No. US20030087818A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Indirias, Carol Yoseph
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Carter, Darick
APPLICANT: Fanger, Gary R.
APPLICANT: Smith, Carole L.
APPLICANT: Durham, Margalita
APPLICANT: Stolk, John A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066.543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 593
LENGTH: 393
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc.feature
LOCATION: 51, 53, 73, 91, 121, 128, 167, 177, 216, 225, 245, 265, 281,
LOCATION: 295, 306, 313, 333, 363, 392
OTHER INFORMATION: n = A,T,C or G
US-10-066-543-593

Query Match 9.6%; Score 48.4; DB 14; Length 393;
Best Local Similarity 47.6%; Pred. No. 0.056;
Matches 121; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 253 TTGCTTGTGAAGAAGATCTCAAGCATTAATTAAGTTGATATGATTAAGTCTC 312
DB 274 TTTTTCANAAATTAATTTTAAAGNAAAGGAGAGATTTTAATTAAT 215
QY 313 ACACAAATTAATTAAGTGTGCTTTCTTAAGAGGTAATTAATTAAGTGTATCTT 372
DB 214 GAGCAGAAATTAATCTGTGTATTTGACATTAATTAATTAATTAATTAATTA 155
QY 373 GGTGTATGACCATTTGACACATTAATTAAGTGTGACACATCAATCTTCATGTA 432
DB 154 GCTTTTAATTTTATCAAAATTAATTAAGTGTGATCTACTGTGTAACAGCTTGT 95
QY 433 TCTTATTAAGTTGTGTGTTTAATGAAGAGATCGTTACGGCTTAATAAAAAA 492
DB 94 TCANAACTGATTAATTTCTGTCGTCATTAATTAATTAATTAATTAATTAATTA 35
QY 493 AAAAAAAAAAAAAA 506
DB 34 AAAAAAAAAAAAAA 21

RESULT 6

US-09-925-299-70
Sequence 70, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925.299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556

SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 70
LENGTH: 2682
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (647)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-70

Query Match 9.5%; Score 48; DB 9; Length 2682;
Best Local Similarity 49.2%; Pred. No. 0.16;
Matches 123; Conservative 1; Mismatches 126; Indels 0; Gaps 0;

QY 253 TTGCTTGCTTGAAGAGAGGTTCCCTCAGCAGTAATTAGTTGATTGATTAGTGTGC 312
DB 2433 TTTTTCGAAATATATGTTTAAAAAGACAAAACAAAGGAGATTTTAATTAAT 2492
QY 313 ACACAAATTAATAAAGTGTGCTTTCTTAAAGGGTACTTATATGTTGATTTCT 372
DB 2493 GAGCAGAAAGTAATCTGTGTATTTGTACATTAATTTTATATGATGATTTAT 2552
QY 373 GGTGTATAGTACCATTTGACACATTAATTAAGTTGTGACACATCATCTTCATGTA 432
DB 2553 GCTTTTAAATTTTATATCAAAATTAAGTATGATCTACTGTTATGACAGCTTGT 2612
QY 433 TCTTCTATTAAGTTGTGTGTTTAAAGAAAGATCGTTTACGCTTAAATTTTAA 492
DB 2613 TCATTAACATGTAATTTCTGTGTATTAATTAATTTCAATGTTGAAAAAATA 2672
QY 493 AAAAAAAAAA 502
DB 2673 AAAAAAAAAA 2682

RESULT 7
US-09-925-299-70
Sequence 70, Application US/09925299
Publication No. US20030040617A9
GENERAL INFORMATION:
APPLICANT: Rozen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 70
LENGTH: 2682
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (647)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-70

Query Match 9.5%; Score 48; DB 11; Length 2682;
Best Local Similarity 49.2%; Pred. No. 0.16;
Matches 123; Conservative 1; Mismatches 126; Indels 0; Gaps 0;

QY 253 TTGCTTGCTTGAAGAGAGTTCCTCAGCAGTAATTAGTTGATTGATTAGTGTGC 312
DB 2433 TTTTTCGAAATATATGTTTAAAAAGACAAAACAAAGGAGATTTTAATTAAT 2492
QY 313 ACACAAATTAATAAAGTGTGCTTTCTTAAAGGGTACTTATATGTTGATTTCT 372
DB 2493 GAGCAGAAAGTAATCTGTGTATTTGTACATTAATTTTATATGATGATTTAT 2552

QY 373 GGTGTATAGTACCATTTGACACATTAATTAAGTTGTGACACATCAATCTTCATGTA 432
DB 2553 GCTTTTAAATTTTATATCAAAATTAAGTATGATCTACTGTTATGACAGCTTGT 2612
QY 433 TCTTCTATTAAGTTGTGTGTTTAAAGAAAGATCGTTTACGCTTAAATTTTAA 492
DB 2613 TCATTAACATGTAATTTCTGTGTATTAATTAATTTCAATGTTGAAAAAATA 2672
QY 493 AAAAAAAAAA 502
DB 2673 AAAAAAAAAA 2682

RESULT 8
US-10-106-698-248/c
Sequence 248, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 248
LENGTH: 2682
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (2036) (2036)
OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-248

Query Match 9.5%; Score 48; DB 14; Length 2682;
Best Local Similarity 49.2%; Pred. No. 0.16;
Matches 123; Conservative 1; Mismatches 126; Indels 0; Gaps 0;

QY 253 TTGCTTGCTTGAAGAGGTTCCCTCAGCAGTAATTAGTTGATTGATTAGTGTGC 312
DB 250 TTTTTCGAAATATATGTTTAAAAAGACAAAACAAAGGAGATTTTAATTAAT 191
QY 313 ACACAAATTAATAAAGTGTGCTTTCTTAAAGGGTACTTATATGTTGATTTCT 372
DB 190 GAGCAGAAAGTAATCTGTGTATTTGTACATTAATTTTATATGATGATTTAT 131
QY 373 GGTGTATAGTACCATTTGACACATTAATTAAGTTGTGACACATCATCTTCATGTA 432
DB 130 GCTTTTAAATTTTATCAAAATTAAGTATCTACTACCTACTGTAACAGCTTGT 71
QY 433 TCTTCTATTAAGTTGTGTGTTTAAAGAAAGATCGTTTACGCTTAAATTTTAA 492
DB 70 TCATTAACATGTAATTTCTGTGTATTAATTAATTTCAATGTTGAAAAAATA 11
QY 493 AAAAAAAAAA 502
DB 10 AAAAAAAAAA 1

RESULT 9
US-10-311-455-1249
Sequence 1249, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander

```

Query March 9.3%; Score 47; DB 10; Length 250;
Best Local Similarity 59.3%; Pred. No. 0.098;
Matches 80; Conservative 0; Mismatches 55; Indels 0; Gaps 0

OY 372 TGGTATAGTAGACATTGCACATTTAAATTAAGTTGGACATCAATCCTTCATGT 431
DB 39 TGTGTAGAGTTAGTGTGTTTGGTGTAAACCAATTTGGGAGATGTAAACATTCCTT 98
OY 432 ACCCTCATTAAGTTGTGTGTTTAAATGAAGAAAGAGTCGTTACGGCTAAAAAAAAA 491
DB 99 ATCGTTTATAGCTTAGTCGCCAAAATGAAAATTGACGTTATTTTCCAAAAAAA 158
OY 492 AAAAAAAAAAAAAA 506
DB 159 AAAAAAAAAAAAAA 173

RESULT 12
US-10-198-846-2929/c
; Sequence 2929, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-043
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18

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; TYPE: DNA
; ORGANISM: Homo sapiens

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Best Local Similarity 50.24; Pred. No. 1.2;
Matches 112; Conservative 0; Mismatches 111; Indels 0; Gaps 0

Oy	361	TGTTGTATCTTCGGTGAAGTAGTGACCATTTGACACATAAATTAAAGTTGTGACACATCA	420
Db	361	TGTTGTATCTTCGGTGAAGTAGTGACCATTTGACACATAAATTAAAGTTGTGACACATCA	420
Oy	421	AACCCTCAGTAGATCTCTCTAATTAAGTTGGTGTAAATGAAAAGATCGTTACGGTC	480
Db	421	AACCCTCAGTAGATCTCTCTAATTAAGTTGGTGTAAATGAAAAGATCGTTACGGTC	480
Oy	481	TTTTAAAAAAAAAAAAAAAAAAAAA	506
Db	481	TTTTAAAAAAAAAAAAAAAAAAAAA	506

RESULT 2

Sequence 1, Application US/08984320
Patent No. 6222097
GENERAL INFORMATION:
APPLICANT: Mcbride, Kevin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,320
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087
FILING DATE: 07-JUN-95
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-984-320-1

Query Match	18.54;	Score 93.8;	DB:3;	Length 564;
Best Local Similarity	61.24;	Pred. No. 5.5e-14;		
Matches 330;	Conservative	0;	Mismatches 132;	Indels 77; Gaps 8

8 CTATGGCTGTTCCATTACTTCATGGCATTTCCTTGTCTTGGCAATGACACTCTTGTG 67

Db 38 CCAATGCTCGTTCACATTTTCTTCAATGGCATTTTGGTCTGGCATAATGCTCTTTGTA 97

Qy 68 CTTATGGCGGTGCAGAGCAAGAAATTTGC---TGTAAAGAGCTCACAAAACCTGTAAAT 124

Db 98 CCTATAGGTAGAAAGCTCAGCAAAATTTGGAAAGCACCAAGCAAACTTTCCACAGATTAT 157

Qy 125 GTTCTAGTAGCCCTCTATGTCAAAAACCTGTATGGAGAGAGAAATATGAAGATGTC 184

Db 158 GTTTATAGCACTCATCATGTAGCAAAATTTGTAT---CAAGACAAATTTCTGATGGAC 214

Qy 185 ATGTGTTCAATCCCTAAGCAAGTCTGTATGATGAAGAATGTAAATCTAAACCTCG 244

Db 215 ATGTAGCAAACTCAAGAAAGTGTCTATGACCTAAGCCATGTGTATTGACAAAAATCT 274

Qy 245 CAACAGAAAT-----GCTTGCTTG 265

Db 275 CAAGTAGATTAAAGCACTTGGTAGAGAGCAAAAACCTAAGTAGAAATTTGGCTTG 334

Qy 264 AAGAAGAGTTCCTCAAGCAGTAAT-----TAAGTTGATTATGATTTAGTGT 311

Db 335 AAGAAGAGATTATGATGAGATTAATAATTAAGAGAGTTAAATTAAGAGATTTGAGATGCA 394

Qy 312 --CAACAATAATTAATAAGTGTGCCCTTTCTTAAAGGTAACCTATTAATGTTG--T 366

Db 395 AAAAAACAATAATTAAGAGTGTGCTTTCTTATTAAGGAGTACTGTGTATGTTGGTT 454

Qy 367 ATTCTGGATATAGTAGGCATTGACACATTAATTAAGTGTGACACATCAATCCTT 428

Db 455 AGATTTGGCCTATAGTAGGCATTGACACATTAATTAAGTGTGACACATCAATCATC 513

Qy 427 CATGTATCTTATTAAGTGTGTGCTTTAATGAAGAGATGTTAAGCTGTAAAT 485

Db 514 C-----TATAGTATGATATGTTTAAATGAAGAAATGATGACATCAATCTTTAA 560

RESULT 3

Sequence 1, Application US/0847087A
Patent No. 6268546
GENERAL INFORMATION:
APPLICANT: McBride, Kevin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087A
FILING DATE: 07-JUN-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719

NAME: Carl J. Schvedler
 REGISTRATION NUMBER: 36,924
 REFERENCE/DOCKET NUMBER: CGNE 91-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 564 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-487-087A-1

Query Match 18.5%; Score 93.8; DB 3; Length 564;
 Best Local Similarity 61.2%; Pred. No. 5.5e-14;
 Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;

QY 8 CTATGGCTGCTTCATTTACTGATGCAATTTCTTGGCATGACACTTGTG 67
 DB 38 CATGGCTGCTTCATTTACTGATGCAATTTCTTGGCATGACACTTGTG 97
 QY 68 CTATGGCTGCTTCATTTACTGATGCAATTTCTTGGCATGACACTTGTG 124
 DB 98 CTATGGCTGCTTCATTTACTGATGCAATTTCTTGGCATGACACTTGTG 157
 QY 125 GTTCTAGTACCTCTATGTCATAAATCTGTATGAGAGAGAAATATAGATGTC 184
 DB 158 GTTCTAGTACCTCTATGTCATAAATCTGTATGAGAGAGAAATATAGATGTC 214
 QY 185 ATTGTTGCAATCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 244
 DB 215 ATTGTTGCAATCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 274
 QY 245 CAACAGATTT-----GCTTCTTG 263
 DB 275 CAAGTAACTTAAAGCACTTGGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 334
 QY 264 AAGAAAGTTCTCAAGCAATTT-----TAAGTTGATTAAGATTAAGT----- 311
 DB 335 AAGAAAGTTCTCAAGCAATTT-----TAAGTTGATTAAGATTAAGT----- 394
 QY 312 --CACCAAAATTAATAAAGTGTGCTTCTTAAAGGTAATTAATGTTG--T 366
 DB 395 AAAAAAATAATTAATAAAGTGTGCTTCTTAAAGGTAATTAATGTTG--T 454
 QY 367 ATTCTGGTATGATGAGCAATTTGACACATTAATTAAGTTGTGACATCAATCCTT 426
 DB 455 AGATTGGCTTATGATGAGCAATTTGACACATTAATTAAGTTGTGACATCAATC 513
 QY 427 CATGATCTTCTATTAAGTTGTGTTTAAAGAAAGAGAGAGAGAGAGAGAGAG 485
 DB 514 C-----TTATGATGATGATGTTTAAAGAAAGAGAGAGAGAGAGAGAGAG 560

RESULT 4
 US-08-397-653B-1
 Sequence 1, Application US/08397653B
 Patent No. 6329570
 GENERAL INFORMATION:
 APPLICANT: Martineau, Belinda
 TITLE OF INVENTION: COTTON MODIFICATION USING
 TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL
 TITLE OF INVENTION: FACTORS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESS: Calgene, Inc.
 STREET: 1920 Fifth Street
 CITY: Davis
 STATE: CA
 COUNTRY: USA
 ZIP: 95616

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.0
 SOFTWARE: Microsoft Word 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/397,653B
 FILING DATE: 28-FEB-1995
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth Lassen
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 NAME: Carl J. Schvedler
 REGISTRATION NUMBER: 36,924
 REFERENCE/DOCKET NUMBER: CGNE 112
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 564 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-397-653B-1

Query Match 18.5%; Score 93.8; DB 4; Length 564;
 Best Local Similarity 61.2%; Pred. No. 5.5e-14;
 Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;

QY 8 CTATGGCTGCTTCATTTACTGATGCAATTTCTTGGCATGACACTTGTG 67
 DB 38 CATGGCTGCTTCATTTACTGATGCAATTTCTTGGCATGACACTTGTG 97
 QY 68 CTATGGCTGCTTCATTTACTGATGCAATTTCTTGGCATGACACTTGTG 124
 DB 98 CTATGGCTGCTTCATTTACTGATGCAATTTCTTGGCATGACACTTGTG 157
 QY 125 GTTCTAGTACCTCTATGTCATAAATCTGTATGAGAGAGAAATATAGATGTC 184
 DB 158 GTTCTAGTACCTCTATGTCATAAATCTGTATGAGAGAGAAATATAGATGTC 214
 QY 185 ATTGTTGCAATCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 244
 DB 215 ATTGTTGCAATCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 274
 QY 245 CAACAGATTT-----GCTTCTTG 263
 DB 275 CAAGTAACTTAAAGCACTTGGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 334
 QY 264 AAGAAAGTTCTCAAGCAATTT-----TAAGTTGATTAAGATTAAGT----- 311
 DB 335 AAGAAAGTTCTCAAGCAATTT-----TAAGTTGATTAAGATTAAGT----- 394
 QY 312 --CACCAAAATTAATAAAGTGTGCTTCTTAAAGGTAATTAATGTTG--T 366
 DB 395 AAAAAAATAATTAATAAAGTGTGCTTCTTAAAGGTAATTAATGTTG--T 454
 QY 367 ATTCTGGTATGATGAGCAATTTGACACATTAATTAAGTTGTGACATCAATCCTT 426
 DB 455 AGATTGGCTTATGATGAGCAATTTGACACATTAATTAAGTTGTGACATCAATC 513
 QY 427 CATGATCTTCTATTAAGTTGTGTTTAAAGAAAGAGAGAGAGAGAGAGAGAG 485
 DB 514 C-----TTATGATGATGATGTTTAAAGAAAGAGAGAGAGAGAGAGAGAG 560

RESULT 5
 5175095-1
 Patent No. 5175095

APPLICANT: Martineau, Belinda M.; Houck, Catherine M.
TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS

NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/554,195

FILING DATE: 17-JUL-1990

SEQ ID NO:1:

LENGTH: 564

Query Match 18.5%; Score 93.8; DB 6; Length 564;
Best Local Similarity 61.2%; Pred No. 5.5e-14;
Matches 330; Conservative 0; Mismatches 133; Indels 77; Gaps 8;

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Qy 8 CTATGCTGCTTCATTTAATTCATGAGCAATTTCTTCTTGGCAATGACCTCTTTGTTG 67
Db 38 CCAATGGCTGCTTCATTTAATTCATGAGCAATTTCTTCTTGGCAATGACCTCTTTGTTA 97
Qy 68 CTATGAGGAGCAAGCAAGAAATTTGCT--TGTAAAGGCTCACAAGAACTCTTAAAT 124
Db 98 CCAATGAGGAGCAAGCAAGAAATTTGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 157
Qy 125 GTTCTAGTGAACCTCTATGTCAAAACTCTGTATGAGAGAGAGAGAAATATGAAGATGTC 184
Db 158 GTTCTATGAGCTCATCATGATAAAATATGTAT--CAAGAGAAATTTACTGTGTGAC 214
Qy 185 ATTGTTCAAGATCTTAAGCAAGTCTTATGATGAGAGATGTAAATGCTAAACCTCG 244
Db 215 ATTGTAAGCAAGCTCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 274
Qy 245 CAACAGAAAT-----GCTTCTTG 263
Db 275 CAAGTAAGTAAGCAAGCAAGTCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 334
Qy 264 AAGAAGGTTCTCAAGCAGTAAT-----TAAGTTGATTATGATTAAGT----- 311
Db 335 AAGAAGGATTAAGTGAAGTAAATTAAGTGAAGTAAATTAAGTGAAGTGAAGTGAAGTGA 394
Qy 312 --CAACAAATTAATTAAGTGTGCTTCTTAAAGGTAATTAATTAAGTGTG--T 366
Db 395 AAAAAAATAATTAATTAAGTGTGCTTCTTAAAGGTAATTAAGTGTGCTTCTTAAAGGTA 454
Qy 367 ATTCTGATGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 426
Db 455 AAGATGGGCTAATGAGCAATTAAGCAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 513
Qy 427 CATGTATCTTATTAAGTGTGCTTCTTAAAGGTAATTAAGTGAAGTGAAGTGAAGTGA 485
Db 514 C-----TTATGTATGATTAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 560

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RESULT 6

US-08-984-320-2
Sequence 2, Application US/08984320

PATENT No. 6223097

GENERAL INFORMATION:

APPLICANT: McBride, Kevin E.

APPLICANT: Stalker, David M.

TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Calgene, Inc.

STREET: 1920 Fifth Street

CITY: Davis

STATE: CA

COUNTRY: USA

ZIP: 95616

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB

OPERATING SYSTEM: Macintosh 7.1

SOFTWARE: Microsoft Word 5.1 (a)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/984,320

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/487,087

FILING DATE: 07-JUN-95

APPLICATION NUMBER: USSN 07/998,158

FILING DATE: 29-DEC-92

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 07/554,195

FILING DATE: 17-JUL-90

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 07/382,518

FILING DATE: 19-JUL-89

ATTORNEY/AGENT INFORMATION:

NAME: Donna E. Scherer

REGISTRATION NUMBER: 34,719

NAME: Carl J. Schwedler

REGISTRATION NUMBER: 36,924

REFERENCE/DOCKET NUMBER: CGNE 91-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (916) 753-6313

TELEFAX: (916) 753-1510

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3528 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

US-08-984-320-2

Query Match 12.4%; Score 62.6; DB 3; Length 3528;

Best Local Similarity 64.8%; Pred. No. 2.4e-06;

Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;

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Qy 262 TGAAGAAGTTCCTCAGCAGTAATTAAGTGTATTAAGTGTATTAAGTGTATTAAGTGTAT 321
Db 3165 TGAAGAAGTAATTAATTAAGTGTATTAAGTGTATTAAGTGTATTAAGTGTATTAAGTGT 3224
Qy 322 TAAATAAAGTGTGCTTCTTAAAGGTAATTAATTAAGTGTATTAAGTGTATTAAGTGT 378
Db 3225 TAAATAAAGTGTGCTTCTTAAAGGTAATTAAGTGTATTAAGTGTATTAAGTGTATTAAG 3284
Qy 379 TAGTAGCATTGAACATTAATTAAGTGTGACATCAATCCTTATGATTAATCTCT 438
Db 3285 TAGTAGCATTGAACATTAATTAAGTGTGACATCAATCCTTATGATTAATCTCT 3332
Qy 439 ATTAAGTGTGTGTTTAAATGAAGAAGATCGTTTACGGTCTAAA 485
Db 3333 -TTATGTATGATGTTTAAATGAAGAAGATCGATCAATCTTTAA 3378

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RESULT 7

US-08-487-087A-2
Sequence 2, Application US/08487087A

PATENT No. 6268546

GENERAL INFORMATION:

APPLICANT: McBride, Kevin E.

APPLICANT: Stalker, David M.

TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Calgene, Inc.

STREET: 1920 Fifth Street

CITY: Davis

STATE: CA

COUNTRY: USA

ZIP: 95616

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB

OPERATING SYSTEM: Macintosh 7.1

SOFTWARE: Microsoft Word 5.1

CURRENT APPLICATION DATA:

SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087A
FILING DATE: 07-JUN-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-487-087A-2

Query Match 12.4%; Score 62.6; DB 3; Length 3528;
Best Local Similarity 64.8%; Pred. No. 2.4e-06;
Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;
Db 262 TGAAGAAGTTCCTCAAGCAGTAATTAAGTTGATTAAGATTAGTGCACACAAAT 321
3165 TGATGAGTAATTAATTAAGTGAAGTTAAGATTAGTGCACACAAAT 3224
Qy 322 TAATAAAGTGTGCTTTCTTAAGAGGTAATTAATGTTGATTC---TTGGTGA 378
Db 3225 TAAATAAGTGTGCTTTCTTAAGAGGTAATTAATGTTGATTC---TTGGTGA 378
Qy 379 TACTAGCCATTGACACATTAATTAAGTTGACACATCAATCCTTCATGATCTTCT 438
Db 3285 TACTAGCCATTGACACATTAATTAAGTTGACACATCAATCCTTCATGATCTTCT 438
Qy 439 ATTAAGTGTGCTTTCTTAATGAAGAAGATCGTTTACGCTTAA 485
Db 3333 -TTATGATGATGTTTAAATGAAGAAATGATCGATCGATCTTAA 3378

RESULT 8
US-08-397-653B-2
Sequence 2, Application US/08397653B
Patent No. 6329570
GENERAL INFORMATION:
APPLICANT: Martineau, Belinda
TITLE OF INVENTION: COTTON MODIFICATION USING
TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL
TITLE OF INVENTION: FACTORS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,653B
FILING DATE: 28-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Larsen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-397-653B-2

Query Match 12.4%; Score 62.6; DB 4; Length 4383;
Best Local Similarity 64.8%; Pred. No. 2.5e-06;
Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;
Db 262 TGAAGAAGTTCCTCAAGCAGTAATTAAGTTGATTAAGATTAGTGCACACAAAT 321
3165 TGATGAGTAATTAATTAAGTGAAGTTAAGATTAGTGCACACAAAT 3224
Qy 322 TAATAAAGTGTGCTTTCTTAAGAGGTAATTAATGTTGATTC---TTGGTGA 378
Db 3225 TAAATAAGTGTGCTTTCTTAAGAGGTAATTAATGTTGATTC---TTGGTGA 378
Qy 379 TACTAGCCATTGACACATTAATTAAGTTGACACATCAATCCTTCATGATCTTCT 438
Db 3285 TACTAGCCATTGACACATTAATTAAGTTGACACATCAATCCTTCATGATCTTCT 438
Qy 439 ATTAAGTGTGCTTTCTTAATGAAGAAGATCGTTTACGCTTAA 485
Db 3333 -TTATGATGATGTTTAAATGAAGAAATGATCGATCGATCTTAA 3378

RESULT 9
5175095-4
Patent No. 5175095
APPLICANT: Martineau, Belinda M.; Houck, Catherine M.
TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/554,195
FILING DATE: 17-JUL-1990
SEQ ID NO: 4
LENGTH: 4383
Query Match 12.4%; Score 62.6; DB 6; Length 4383;
Best Local Similarity 64.8%; Pred. No. 2.5e-06;
Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;
Db 262 TGAAGAAGTTCCTCAAGCAGTAATTAAGTTGATTAAGATTAGTGCACACAAAT 321
3165 TGATGAGTAATTAATTAAGTGAAGTTAAGATTAGTGCACACAAAT 3224
Qy 322 TAATAAAGTGTGCTTTCTTAAGAGGTAATTAATGTTGATTC---TTGGTGA 378
Db 3225 TAAATAAGTGTGCTTTCTTAAGAGGTAATTAATGTTGATTC---TTGGTGA 378
Qy 379 TACTAGCCATTGACACATTAATTAAGTTGACACATCAATCCTTCATGATCTTCT 438

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Page 6

Db 3285 TAGTACCCATTGGACACATTAATC----- 3332

Dy 439 ATTAAGTTGTGTTTAAAGAAAAGATCGTTTACGGTCTAAAA 485

Db 3333 -TTATGTATGATGTTTAAAGAAAAGATCGATCTTTAA 3378

RESULT 10
5177307-1
; Patent No. 5177307
; APPLICANT: HOUCK, CATHERINE M.; PEAR, JULIE R.; MARTINEAU,
; BELINDA M.; HATT, WILLIAM
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; MODULATIONS OF ENDOGENOUS CYTOKININ LEVELS
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/554,196
; FILING DATE: 17-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 362,802
; FILING DATE: 19-JUL-1989
; APPLICATION NUMBER: 188,361
; FILING DATE: 29-APR-1988
; APPLICATION NUMBER: 168,190
; FILING DATE: 15-MAR-1988
; APPLICATION NUMBER: 54,369
; FILING DATE: 26-MAY-1987
; SEQ ID NO:1:
; LENGTH: 4383
; 5177307-1

Query Match	12.4%	Score 62.6	DB 6	Length 4383
Best Local Similarity	64.8%	Pred. No. 2.5e-06		
Matches 147	Conservative	0	Mismatches 64	Indels 16
				Gaps 3
Qy	262	TGMAAGAGGTCCCAAGCAGTAAATPAGTTGATTATGAGATTAGTGTGACACAAAT		321
Db	3165	TCATGAGTAATTAATTAAGTAGGTAAATAGGATTTTGAGTGTCAAAAAACAAAT		3224
Qy	322	TAAATPAAATGTGGCTTTTAAAGGTAACTPAAATGTGTATTC---TGTGTGA		378
Db	3225	TATTAAGGTGTGCTTTTCTTATTAAGGAGCTGTGATGTGTGTTAGTATATGGCTTA		3284
Qy	379	TAGTACCATTTGACACTTAATTAATTAAGTTGTGACACATCAATCTCTATGTATCTCT		438
Db	3285	TAGTACCATTTGACACTTAA--TAAAGTTGTGACACATCAATTAATTC-----		3332
Qy	439	ATTAAATTGTGTGTTTAAATGAAGAAGATCTTTACGCTTAA		485
Db	3333	-TTAATGATATATGTTTAAATGAAGAAATGATCACTACATCTTTAA		3378

RESULT 11
US-08-171-365-14/c
Sequence 14, Application US/08171365
Patent No 5527864
GENERAL INFORMATION:
APPLICANT: Mary E. Russell
APPLICANT: Urike Utans
TITLE OR INVENTION: Mediators of Chronic Allograft
TITLE OF INVENTION: Rejection
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X

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1  OPERATING SYSTEM: MS-DOS (Version 5.0)
2  SOFTWARE: Wordperfect (Version 5.1)
3  CURRENT APPLICATION DATA:
4  APPLICATION NUMBER: US/08/171,385
5  FILING DATE:
6  CLASSIFICATION: 514
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER:
9  FILING DATE:
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Fraser, Jans K.
12 REGISTRATION NUMBER: 34,819
13 REFERENCE/DOCKET NUMBER: 05433/006001
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: (617) 542-5070
16 TELEFAX: (617) 542-8906
17 TELETEX: 200154
18 INFORMATION FOR SEQ. ID NO. 14:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 350
21 TYPE: nucleic acid
22 STRANDEDNESS: double
23 TOPOLOGY: linear
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Query Match	9.0%	Score	45.4	DB 1	Length	350		
Best Local Similarity	53.0%	Pred. No.	0.02					
Matches	97	Conservative	0	Mismatches	86	Indels	0	
							Gaps	0
QY	324	ATATAAAGTTCCTCTCTTAAAGGTAAGTAATATGTTATCTTGAGTATAGTA	383					
DB	194	ATTAAAGGTAAATTTATATATATAGAAAGACATGCTGTTCTTATCTCAGCTCG	135					
QY	384	GCCATTGACACATTAAATTTAAAGTGTGACATCAATCCCTCAGTATCTTATTA	443					
DB	134	ATTATTTTGCTATATATTAATATATTCAGATCCATCAATTTTCTATAGTTGTAAAT	75					
QY	444	GTTTGTGCTTTAATGAAAGACATCGTTACGGCTCAAAAAAAAAAAAAAAAAAAAA	503					
DB	74	TTTCATTATAGCTAAATATAATACTGTGTATGTAAAAAATAAAAAAAAAAAAA	15					
QY	504	AAA 506						
DB	14	AAA 12						

RESULT 12
 US-08-361-441B-14/C
 Sequence 14, Application US/08361441B
 Patent No. 607794B
 GENERAL INFORMATION:
 APPLICANT: Russell, Mary E.
 APPLICANT: Utans, Ulrike
 TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Pasteo for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/361,441B
 FILING DATE: 21-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/171,385
 FILING DATE: 21-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 05433/014001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 350 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-361-441B-14

Query Match

Best Local Similarity 53.0%; Score 45.4; DB 3; Length 350;

Matches 97; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Db

Qy

194 ATTAAGGTAGTAATTTATATAGAAAGACATGCGTTCTTATTCGAGCTCG 135

Qy

384 GCCATTGACATTAATTAAGTTGACACATCAATCCTTCATGATCTTATTA 443

Db

134 ATTAATTTGCTCATATTAATTAATTCAGATCCATCAATTTTCTATAGTTGATAT 75

Qy

444 GTTGTGTTTAAATGAAGAGATCGTTACGCTMAAAAAAAAAAAAAAAAAA 503

Db

74 TTCATTATGCTAAATTAATTAATTCGATCTGTGATGTAATAAAAAAAAAAAAAA 15

Qy

504 AAA 506

Db

14 AAA 12

RESULT 13

US-08-171-385-27/c

Sequence 27, Application US/08171385

Patent No. 5527884

GENERAL INFORMATION:

APPLICANT: Mary E. Russell

APPLICANT: Ulrike Utans

TITLE OF INVENTION: Mediators of Chronic Alllograft

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or SSX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/171.385

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

TELEX: 200154

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 340

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-171-385-27

Query Match

Best Local Similarity 52.5%; Score 43.8; DB 1; Length 340;

Matches 96; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Db

Qy

324 AATTAAGTTCCTTCTTAAAGGTAATTAATGTTATCTTGGTATAGTA 383

Db

196 ATTAAGGTAGTAATTTATATAGAAAGACATGCGTTCTTATTCGAGCTCG 137

Qy

384 GCCATTGACATTAATTAAGTTGACACATCAATCCTTCATGATCTTATTA 443

Db

136 ATTAATTTGCTCATATTAATTAATTCAGATCCATCAATTTTCTATAGTTGATAT 77

Qy

444 GTTGTGTTTAAATGAAGAGATCGTTACGCTMAAAAAAAAAAAAAAAAAA 503

Db

76 TTCATTATGCTAAATTAATTAATTCGATCTGTGATGTAATAAAAAAAAAAAAAA 17

Qy

504 AAA 506

Db

16 AAA 14

RESULT 14

US-08-361-441B-27/c

Sequence 27, Application US/08361441B

Patent No. 6077948

GENERAL INFORMATION:

APPLICANT: Russell, Mary E.

APPLICANT: Utans, Ulrike

TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/361.441B

FILING DATE: 21-DEC-1994

APPLICATION NUMBER: 08/171.385

FILING DATE: 21-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 05433/014001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-361-441B-27

Query Match

Best Local Similarity 52.5%; Score 43.8; DB 1; Length 340;

Matches 96; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Db

Qy

324 AATTAAGTTCCTTCTTAAAGGTAATTAATGTTATCTTGGTATAGTA 383

Db

196 ATTAAGGTAGTAATTTATATAGAAAGACATGCGTTCTTATTCGAGCTCG 137

Qy

384 GCCATTGACATTAATTAAGTTGACACATCAATCCTTCATGATCTTATTA 443

Db

136 ATTAATTTGCTCATATTAATTAATTCAGATCCATCAATTTTCTATAGTTGATAT 77

Qy

444 GTTGTGTTTAAATGAAGAGATCGTTACGCTMAAAAAAAAAAAAAAAAAA 503

Db

76 TTCATTATGCTAAATTAATTAATTCGATCTGTGATGTAATAAAAAAAAAAAAAA 17

Qy

504 AAA 506

Db

16 AAA 14

RESULT 14

US-08-361-441B-27/c

Sequence 27, Application US/08361441B

Patent No. 6077948

GENERAL INFORMATION:

APPLICANT: Russell, Mary E.

APPLICANT: Utans, Ulrike

TITLE OF INVENTION: MEDIATORS OF CHRONIC ALLOGRAFT REJECTION

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/361.441B

FILING DATE: 21-DEC-1994

APPLICATION NUMBER: 08/171.385

FILING DATE: 21-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 05433/014001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

Query Match 8.7%; Score 43.8; DB 3; Length 340;
 Best Local Similarity 52.5%; Pred No. 0.049;
 Matches 96; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

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QY 324 AATTAAGTTGCTTCTTCTTAAGGGTACTTATATGTTGTAATCTTGCTATAGTA 383
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 196 AATTAAGTTGCTTCTTCTTAAGGGTACTTATATGTTGTAATCTTGCTATAGTA 137
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QY 384 GCCATTGACACATTAATTAAGTTGACACATCAATCCTTCATGTAATCTTCTATTA 443
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Db 136 ATTATTTTGTCTATATAATTAATTCAGATCCATCAATTTTCTATTAAGTTGATTAAT 77
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QY 444 GTTGTGTGTTTAAAGAAAGAGATCGTTACGCTTAAAAAATTTTTTTTTTTTTTTT 503
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76 TTCAATTAAGCTTAATAAATAATCTGTGTATGTACTGTAAAAAATTTTTTTTTTTT 17
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QY 504 AAA 506
    |||
Db 16 AAA 14
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RESULT 15
 US-09-388-743-17
 ; Sequence 17, Application US/09388743
 ; Patent No. 6423886
 ; GENERAL INFORMATION:
 ; APPLICANT: Singletary, George
 ; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
 ; FILE REFERENCE: 1144
 ; CURRENT APPLICATION NUMBER: US/09/388,743
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 17
 ; LENGTH: 2274
 ; TYPE: DNA
 ; ORGANISM: *Typha latifolia*
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (115)...(1956)
 US-09-388-743-17

Query Match 8.3%; Score 42; DB 4; Length 2274;
 Best Local Similarity 62.3%; Pred No. 0.19;
 Matches 66; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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QY 401 AATTAAGTTGACACATCAATCTTCATGTAATCTTCTATTAAGTTGTTGTTTAATG 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2159 AATTAATCTCTCTACTCTTCTTAATTAATGCTGTAATGTAATTAATGTAATG 2218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 461 AAAAGAGATGTTAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 506
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Db 2219 AATTAAGCTAAGTTCTTCTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTT 2264
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Search completed: August 23, 2003, 07:04:44
 Job time : 58 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 22:03:51 ; Search time 214 Seconds

(without alignments)
6382.783 Million cell updates/sec

Title: US-09-854-562-1

Perfect score: 506
Sequence: 1 aaagagactatgctcgttc.....aaaaaaaaaaaaaaaaaaaaa 506

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 510512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: N_Geneseq_19Jun03:*
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3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001C.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	506	100.0	506	22 AAF83987	Pepper defensin pr
2	491.6	97.2	548	22 AAX12800	DNA encoding Capsi
3	93.8	18.5	564	12 AAQ10262	Ovary tissue trans
4	93.8	18.5	564	14 AAQ34940	p2130 coding sequ
5	93.8	18.5	564	17 AAT31823	Tomato p2130 cDNA
6	93.8	18.5	564	18 AAT48813	cDNA clone p2130 c
7	93.8	18.5	564	24 ABZ21970	Plasmid p2130 cDNA
8	92	18.2	558	20 AAV70143	Nicotiana panicula

9	92	18.2	566	20 AAV70142	Nicotiana excoelais
10	67.2	13.3	456	20 AAV70141	Nicotiana excoelais
11	62.6	12.4	3528	17 AAT31824	Tomato p2130 genom
12	62.6	12.4	3528	18 AAT48816	Calgene lambda 140
13	62.6	12.4	3528	24 ABZ21971	Plasmid p2130 cDNA
14	62.6	12.4	4383	12 AAQ10263	p2130 contg. Calge
15	62.6	12.4	4383	12 AAQ10319	Calgene lambda 140
16	62.6	12.4	4383	14 AAQ35143	Calgene lambda 140
17	62.6	12.4	4383	14 AAQ34941	Calgene lambda 140
18	50.4	10.0	1210	24 ABV83585	Human breast speci
19	49.8	9.8	7669	24 ABV83585	Human breast speci
20	48.8	9.6	3873	24 ABV83585	Human immune syste
21	48.6	9.6	317	25 ABT22887	Human angiogenesis
22	48	9.5	2682	21 AAC98060	Breast cancer mark
23	48	9.5	2682	22 AAC98060	Human colon cancer
24	47.2	9.3	5675	22 ABV13276	Human colon cancer
25	47	9.3	240	25 ABX25222	Human immune syste
26	47	9.3	250	25 ABX25196	Human GDP-mannose
27	46	9.1	337	22 ABL11578	Human breast cance
28	45.8	9.1	900	22 AAS40950	CDNA encoding nove
29	45.8	9.1	1667	22 AAD18352	Human lipid metabo
30	45.6	9.0	570	22 AAH10998	Human CDNA sequenc
31	45.6	9.0	2751	22 AAH17678	Human CDNA sequenc
32	45.4	9.0	350	16 AAQ93380	Rat allograft infl
33	45.4	9.0	350	21 AAQ56600	Rat allograft infl
34	45.4	9.0	9510	22 AAS46437	Tumour suppressor
35	45.4	9.0	9510	22 ABL34562	Human metastasis a
36	45.2	8.9	427	23 ABV08871	Human prostate exp
37	45.2	8.9	462	23 ABV38762	Human prostate exp
38	45.2	8.9	6074	24 ABK33991	Human DNA for stag
39	45	8.9	205	22 AAS40949	Human cervical can
40	44.8	8.9	921	22 AAS40949	CDNA encoding nove
41	44.4	8.8	278	22 AAH69999	Human cervical can
42	44.4	8.8	375	22 ABV44911	Human prostate exp
43	44	8.7	6022	23 AAS44661	Tumour suppressor
44	43.8	8.7	340	16 AAQ93393	Rat allograft infl
45	43.8	8.7	340	21 AAS46613	Rat allograft infl

ALIGNMENTS

RESULT 1	
AAAF83987	
ID	AAAF83987 standard; cDNA to mRNA; 506 BP.
AC	AAAF83987;
XX	
DT	22-AUG-2001 (first entry)
DE	Pepper defensin protein gene, PeppDef cDNA sequence.
XX	
KW	Pepper; defensin; PeppDef; thionin-like protein; PeppH1; transgenic;
KW	phytopathogen; antimicrobial; ss.
XX	
OS	Capsicum annuum.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	/*tag= a
FT	/product= "defensin protein"
FT	/gene= "PeppDef"
XX	
PN	EP1101771-A1.
XX	
PD	23-MAY-2001.
XX	
PF	15-NOV-1999; 99EP-0309059.
XX	
PR	15-NOV-1999; 99EP-0309059.
XX	
PA	(KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX	

Nicotiana excoelais
Nicotiana excoelais
Tomato p2130 genom
Calgene lambda 140
Plasmid p2130 cDNA
p2130 contg. Calge
Calgene lambda 140
Calgene lambda 140
Human breast speci
Human immune syste
Human angiogenesis
Breast cancer mark
Human colon cancer
Human colon cancer
Human immune syste
Human GDP-mannose
Human GDP-mannose
Human breast cance
CDNA encoding nove
Human lipid metabo
Human CDNA sequenc
Human CDNA sequenc
Rat allograft infl
Rat allograft infl
Tumour suppressor
Human metastasis a
Human prostate exp
Human prostate exp
Human DNA for stag
Human cervical can
CDNA encoding nove
Human cervical can
Human prostate exp
Tumour suppressor
Rat allograft infl
Rat allograft infl

Pt	Oh B,	Ko MK,	Shin B,	Chung CH;
DR	WPI:	2001-357927/38.		
DR	p-PsDB:	AAB85079.		
XX	New pathogen induced genes (pepper defensin protein gene and pepper			
PT	thionin-like protein gene) from Capsicum annuum, useful for producing			
PT	transgenic plants with enhanced resistance against phytopathogens, e.g.			
XX	fungi or nematode	-		
PS	Claim 3; Page 10-11.; 22pp; English.			
CC	The invention provides new isolated nucleic acid molecules encoding a			
CC	pepper defensin protein (Pepdef) and a pepper thionin-like protein			
CC	(PepThn). The Pepdef and PepThn genes are useful for producing transgenic			
CC	plants that exhibit enhanced resistance against phytopathogens, e.g.			
CC	fungi, bacteria, viruses, nematode, mycoplasma-like organisms, parasitic			
CC	higher plants, flagellate protozoa or insects. The present sequence			
CC	represents the cDNA sequence of the Pepdef gene.			
SQ	Sequence 506 BP; 174 A; 74 C; 96 G; 162 T; 0 other;			
Query Match	100.0%; Score 506; DB 22;	Length 506;		
Best Local Similarity	100.0%; Pred. No. 3.9e-98;			
Matches 506;	Conservative 0; Mismatches 0;	Indels 0; Gaps 0;		
OY	1 AAAGAGCATATGGCTGTTGCATTACTTCATCGCATTCTTGCTTGGCAATGACATC	60		
Dd	1 AAAGAGCATATGGCTGTTGCATTACTTCATCGCATTCTTGCTTGGCAATGACATC	60		
OY	61 TTGTGTTGCTTAATGGGCTGTGCAAGGCAAGAAATTTGCTGTAAAGACTCACAAA	120		
Dd	61 TTGTGTTGCTTAATGGGCTGTGCAAGGCAAGAAATTTGCTGTAAAGACTCACAAA	120		
OY	121 AAATGTTCTAAGTACCCTCTATGCTCAAAAACTGTATAGGAAGAATAATGAAAT	180		
Dd	121 AAATGTTCTAAGTACCCTCTATGCTCAAAAACTGTATAGGAAGAATAATGAAAT	180		
OY	181 GGTCATTTGTTTCAATCTTAAGCAAGTGTCTTATGATGAAGATGTAATGCTAAAT	240		
Dd	181 GGTCATTTGTTTCAATCTTAAGCAAGTGTCTTATGATGAAGATGTAATGCTAAAT	240		
OY	241 CTGCAACAAGAAATGGTCTCTTGAAGAAGATGCTCAAGCAGTAATTAAGTTGATAT	300		
Dd	241 CTGCAACAAGAAATGGTCTCTTGAAGAAGATGCTCAAGCAGTAATTAAGTTGATAT	300		
OY	301 GGATTAGTGTACACAAATTAAATTAAGTGTGCTTTCTTAAAGGTTAATTATA	360		
Dd	301 GGATTAGTGTACACAAATTAAATTAAGTGTGCTTTCTTAAAGGTTAATTATA	360		
OY	361 TGTTGTAATCTTGGTATAGTAGCATTTTGACATTAATTAAGTTGTGACATCA	420		
Dd	361 TGTTGTAATCTTGGTATAGTAGCATTTTGACATTAATTAAGTTGTGACATCA	420		
OY	421 ATCTTCATATGTCTTCTCTATTAAGTTGTGTGTTTAATGAAAAAGATGTTTACGTC	480		
Dd	421 ATCTTCATATGTCTTCTCTATTAAGTTGTGTGTTTAATGAAAAAGATGTTTACGTC	480		
OY	481 TAAAAAATTT	506		
Dd	481 TAAAAAATTT	506		
RESULT 2	ABX12800 standard; DNA; 548 BP.			
XX	ABX12800;			
XX	ABX12800;			
DT	29-MAY-2003 (first entry)			
XX	DNA encoding Capsicum annuum L. cv. Hanbyul thionine.			

XX	Thionine; plant disease resistance; plant; gene; ds.
OS	Capsicum annuum L. cv. Hanbyul.
XX	
PH	Key
FT	Location/Qualifiers
CD	52..306
FT	/tag= a
FT	/product= "Thionine"
FT	/transl_except= (pos:64..66,aa:Thr)
FT	/transl_except= (pos:271..273,aa:Xaa)
FT	/note= "Xaa is given as "Net" in the specification"
XX	
PN	KR2002024732-A.
XX	
PD	01-APR-2002.
XX	
PP	26-SEP-2000; 2000KR-0056518.
XX	
PR	26-SEP-2000; 2000KR-0056518.
XX	
PA	(KOCH-) KOREA CHUNGANG EDUCATIONAL FOUND.
XX	
P1	Hwang BG, Kim YJ, Lee SC;
DR	WPI; 2002-747901/81.
DR	P-PSDB; ABU08325.
XX	
PT	Thionine gene of capsicum annuum l. cv. hanbyul and probing method of
PT	resistance for plant diseases -
XX	
PS	Example 1; Fig 1; 14pp; Korean.
XX	
CC	The present invention relates to the thionine gene of Capsicum
CC	annuum L. cv. Hanbyul, and a probing method of resistance for
CC	plant diseases, caused by Xanthomonas campestris subsp. vesicatoria,
CC	Collectotrichum coccodes, Collectotrichum gloeosporioides and the like.
CC	The presents sequence encodes Capsicum annuum L. cv. Hanbyul thionine.
XX	
SO	Sequence 548 BP; 188 A; 76 C; 105 G; 179 T; 0 other;
<hr/>	
Query Match	97.2%; Score 491.6; DB 24; Length 548;
Best local Similarity	98.2%; Pred. No. 4.4e-95;
Matches 497; Conservative	0; Mismatches 9; Indels 0; Gaps 0;
<hr/>	
OY	1 AAGAGACATGSGCTGGTTCATTACTCATGTGCATTTCTTGTCGCAATGACACTC 60
Db	43 AAGAAGACATGSGCTCGTTCATTACTCATGTGCATTTCTTGTCGCAATGACACTC 102
OY	61 TTGTGGCTTAATGGGSGTSCAAGGCAAGAAATTTGCTGAAGAGCTCACAAAACCTGTT 120
Db	103 TTGTGGCTTAATGGGSGTSCAAGGCAAGAAATTTGCTGAAGAGCTCACAAAACCTGTT 162
OY	121 AAATGTTCTAGTAGACCCCTCATATGTCAAAACTCGTATGAGAAAGAAATATGAGAT 180
Db	163 AAATGTTCTAGTAGACCCCTCATATGTCAAAACTCGTATGAGAAAGAAATATGAGAT 222
OY	181 GGTCAATGTTTACAATCTTAAGCAAGTGGCTTATGACATGAAGATGTAATGCTAAACT 240
Db	223 GGTCAATGTTTACAATCTTAAGCAAGTGGCTTATGACATGAAGATGTAATGCTAAACT 282
OY	241 CTGCGAACAGAAATGTCCTGTGAAGAAAGATTTCTCAAGCAGATAATTAAGTTTAAAT 300
Db	283 CTGCGAACAGAAATGTCCTGTGAAGAAAGATTTCTCAAGCAGATAATTAAGTTTAAAT 342
OY	301 GAATTTAGTGTACACAAAATTTAAATAAAGTGTGCTTTCTTAAAGGTTAATCTTAATA 360
Db	343 GGATTTAGTGTACACAAAATTTAAATAAAGTGTGCTTTCTTAAAGGTTAATCTTAATA 402
OY	361 TGATGTAATCTTGAGGTATATAGAGCAATTTGACACATTAATTAAGTTGTGACACATCA 420
Db	403 TGATGTAATCTTGAGGTATATAGAGCAATTTGACACATTAATTAAGTTGTGACACATCA 462
OY	421 ATCCCTTCATGATCTCTTAATTAAGTTGTGTGTTTTAATGAAAAAGATCGTTTACGGTC 480


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Db      463 ATCCCTTCATGATCTCTTATTAAGTTGTGTTTAAATAAGAGATCGTTACGGTTC 522
Qy      481 TAAAAAAAAAAAAAAAAAAAAA 506
Db      523 TATATGTAAAAAAAAAAAAAAAAAAAAA 548

RESULT 3
AAQ10262
ID      AAQ10262 standard; cDNA; 564 BP.
XX
XX      AAQ10262;
AC
XX
XX      25-MAR-2003 (updated)
DT      04-APR-1991 (first entry)
DE      Ovary tissue transcriptional factor DNA clone pz130.
XX
XX      Ovary tissue transcriptional factor; DNA construct; probe;
KM      clone pz130; ds.
XX
XX      Lycopersicon esculentum UC82B.
OS
XX
XX      Key      Location/Qualifiers
FH      misc_feature      447..564
FT      /*tag= a
FT      /label= pz130_probe
XX
XX      BP409629-A.
XX
XX      . 23-JAN-1991.
PD
XX
XX      19-JUL-1990; 90EP-0307926.
PE
XX
XX      19-JUL-1989; 89US-0382518.
PR
XX
XX      (CALJ ) CALGENE INC.
PA
XX
XX      Martineau B, Houck CM;
PI
XX
XX      WPI; 1991-024191/04.
DR      P-PSDB; AAR10310.
XX
XX      New ovary tissue transcriptional factors - modify transcription
PT      in tomato plant ovaries for use as mol. probes
XX
XX      Disclosure; Fig 1; 21pp; English.
PS
XX
XX      The tomato-derived transcriptional initiation region which regulates
CC      the expression of the sequence corresp. to the pz130 clone is
CC      considered ovary-specific. Sequences hybridizable to the pz130
CC      clone, e.g. probe pz7, show abundant mRNA, esp. at the early stages
CC      of anthesis. The message is expressed in ovary, integument and ovary
CC      outer pericarp tissue and is not expressed, or at least not readily
CC      detectable, in other tissues or at any other stage of fruit
CC      development. The native function of the amino acid sequence
CC      encoded by the structural gene comprising pz130 is unknown.
CC      See also AAQ10263-64.
CC      (Updated on 25-MAR-2003 to correct PA field.)
XX
XX      Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;
SQ
Query Match      18.5%; Score 93.8; DB 12; Length 564;
Best Local Similarity 61.2%; Pred. No. 7e-11;
Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;
Qy      8 CTATGGCTGCTTCATTTACTTCATGAGCATTTCTTGTCTGGCAATGACATCTTGTG 67
Db      38 CCAATGGCTGCTTCATTTCTTCATGAGCATTTTGTCTGGCAATGACATCTTGTGTA 97
Qy      68 CTATGGGCTGCAAGCAAGAAATTTGC---TGTAAAGCTCACAAACCTGTAAAT 124

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Db      98 CCTATGAGTAGAAGCTCAGCAAAATTTGCAAGCACCAACCAACTTCCAGAGATTAT 157
Qy      125 GTTCTAGTAGACCTCTTATGTCAAAACCTGTATGAGAGAGAAATATGAAATGTC 184
Db      158 GTTTTATGAGACTCATCATGTAGAAAATATTGTAT---CAAAGGAAATTTACTGCTGAC 214
Qy      185 ATTTGTTCACAATCTTAAGCAAGCTTATGATGAGAGATGTAATGCTAAACTTCG 244
Db      215 ATTGTAGCAAACTCCAAAGGAAGTGTATGACATAAGCCATGTATTTGCAAAATCT 274
Qy      245 CAACAGAAAT-----GCTTGCTTG 263
Db      275 CAAGTGAAGTTAAAGCACTTGGGTAGAGAACAAAACCTTAAGTGAAGTTGCTTG 334
Qy      264 AAGAGAGTCTCTCAGAGATAAT-----TAGTTGATTAAGATTACTGT----- 311
Db      335 AAGAAAGATTATATGATGAGTAATTAATGAAGTAAATTAAGATTTTAAGTCA 394
Qy      312 --CACCAAAATTAATTAAGTGTGCTTCTTAAAGGTAACCTTAATATGTTG---T 366
Db      395 AAAAAACAAATTAATTAAGTGTGCTTCTTAAAGGTAACCTTGAATGTTGTT 454
Qy      367 ATTTCTGCTATAGTACCATTTGACATTAATTAAGTGTGACATCAATCTCT 426
Db      455 AGTATTTGGCTATAGTACCATTTGACACATTAATTAAGTGTGACATCAATTAATC 513
Qy      427 CATGTATCTTCTATTAACTTTGTGTGTTTAATGAAGAGATCGTTTACGGTCAAAA 485
Db      514 C-----TTATGTATGATATGTTTAAATGAAGAAATGATCGACTACATCTTAA 560

RESULT 4
AAQ34940
ID      AAQ34940 standard; DNA; 564 BP.
XX
XX      AAQ34940;
AC
XX
XX      25-MAR-2003 (updated)
DT      19-MAY-1993 (first entry)
DE      pz130 coding sequence.
XX
XX      cDNA; clone pz130; anthesis; tomato; ovary; integument; outer pericarp;
KM      fruit; development; transcription; initiation; region; modulation;
KM      ovary-specific; endogenous; fruit product; exogenous; phenotype; ds.
XX
XX      Lycopersicon esculentum.
OS
XX
XX      Key      Location/Qualifiers
FH      misc_RNA      447..564
FT      /*tag= a
FT      /note= "Corresponds to pz7 cDNA"
XX
XX      US5175095-A.
PD
XX
XX      29-DEC-1992.
XX
XX      17-JUL-1990; 90US-0554195.
PE
XX
XX      19-JUL-1989; 89US-0382518.
PR      17-JUL-1990; 90US-0554195.
XX
XX      (CALJ ) CALGENE INC.
PA
XX
XX      Houck CM, Martineau BM;
PI
XX
XX      WPI; 1993-026940/03.
DR      P-PSDB; AAR30779.
XX
XX      DNA constructs contg. tomato pz130 transcriptional initiation
PT      region - useful for modulation of endogenous fruit prods. and for
PT      prodn. of exogenous prods.
XX

```

PS Disclosure; Fig 1; 18pp; English.

XX The sequence given shows the DNA sequence of cDNA clone pz130. This
CC sequence is expressed during the early stages of anthesis in tomato.
CC The message is expressed in ovary integument and ovary outer pericarp
CC tissue. It is not readily detectable in other tissues or at other
CC stages of fruit development. The transcription initiation region
CC associated with this gene is therefore considered to be ovary-
CC specific. The actual function of the pz130 polypeptide is unknown.
CC The transcription initiation region can be used for modulation of
CC endogenous fruit products, for production of exogenous products and
CC for modification of the phenotype of fruit and fruit products.
CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;

Query Match 18.5%; Score 93.8; DB 14; Length 564;
Best Local Similarity 561.2%; Pred. No. 7e-11;
Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;

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QY      8 CTATGCTGCTTCATTTACTTCATGCGATTTCTTCTTGGCAATGACCTCTTTGTTG 67
DB      38 CCAATGCTGCTTCATTTACTTCATGCGATTTCTTCTTGGCAATGACCTCTTTGTTA 97
QY      68 CTATGAGGTGAGCAAGCAAGAAATTTGC--TGTAAAGAGCTCACAACAACTGTTAAAT 124
DB      98 CCAATGAGGTGAGCAAGCAAGAAATTTGC--TGTAAAGAGCTCACAACAACTGTTAAAT 157
QY      125 GTTCTGATGACCTCTATGTCACAACTCTGTATGAGAGAGAAATATGAAATGTC 184
DB      158 GTTCTGATGACCTCTATGTCACAACTCTGTATGAGAGAGAAATATGAAATGTC 214
QY      185 ATTTGTTCACAATCTTAAGCAAGTCTTATGATGAGAGATGATGCTAAACCTCTG 244
DB      215 ATTTGTTCACAATCTTAAGCAAGTCTTATGATGAGAGATGATGCTAAACCTCTG 274
QY      245 CAACGAAT-----GCTGCTTG 263
DB      275 CAAGTAAAGTTAAAGCAACTTGGGTGAGAGCAAAACCTTAAGTAAAGTTGCTTG 334
QY      264 AAGAAGAGTCTCAAGCAAGTAAT-----TAAATTGATTAAGTAAAGT----- 311
DB      335 AAGAAGAGTATGATGAGATTAATTAAGTAAAGTAAATTAAGATTTGAGTCA 394
QY      312 --CAACAAATTAATTAAGTGTGCTTCTTAAGGTAACCTTAATATGTTG--T 366
DB      395 AAAAAACAAATTAATTAAGTGTGCTTCTTATTAAGGTAACCTTATGATGTGTT 454
QY      367 ATTTGTTGATTAAGTATGACATTTGACATTAATTAAGTGTGACATCATCTT 426
DB      455 AGTATGAGCTTATGAGCAATTTGACATTAAT--TAAATTGATGACATCATTAATC 513
QY      427 CATGATCTTCTTAATTAAGTGTGTTTAAATAAGAGATGCTTAAAGGCTTAA 485
DB      514 C-----TATGATGATTAATTAATAAATGATGACTAGATCTTTAA 560

```

RESULT 5

AAT31823 standard; cDNA; 564 BP.

XX AAT31823;

XX 25-MAR-2003 (updated)

XX 14-SEP-1996 (first entry)

XX Tomato pz130 cDNA clone.

XX Ovary; ovule; fruit; tomato; cotton; melanin; vector;

XX transgenic plant; ss.

XX Lycopersicon esculentum cv. UC82B.

PH Key Location/Qualifiers

FT CDS 1..357

/*tag= a

XX US5530185-A.

XX 25-JUN-1996.

XX 29-DEC-1992; 92US-0998158.

XX 23-DEC-1992; 92US-0998158.

XX 19-JUL-1989; 89US-0382518.

XX 17-JUL-1990; 90US-0534195.

XX (CALY) CALGENE INC.

XX Martineau BM, Reilley AA, Stalker DM;

XX WPI: 1996-108822/31.

XX P-PSDB; AAR97559.

XX DNA construct for expressing melanin synthesis gene in plant ovule

XX cells - contains promoter from the tomato pz130 gene, also binary

XX vector and transgenic plants, esp. cotton, contg. construct

XX Example 3; Fig 1A-B; 25pp; English.

CC The tomato pz130 clone contains a 564 bp insert of cDNA (AAT31823)
CC detected only in a tomato cDNA library prepd. from pre-anthesis
CC RNA. It was isolated by screening a library prepd. from cDNA
CC of pre-anthesis stage ovaries with probes made from pre-anthesis
CC mRNA, leaf mRNA and young seedling mRNA. The insert was used to
CC isolate the corresponding genomic clone (AAT31824). The pz130
CC transcriptional initiation region is considered to be ovary-specific.
CC It can be utilised in DNA constructs for the expression of
CC heterologous genes, partic. in early fruit development, and esp. for
CC expression of a melanin synthesis gene in transgenic cotton. The
CC native function of the pz130 gene product (AAR97559) is unknown.
CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;
Query Match 18.5%; Score 93.8; DB 17; Length 564;
Best Local Similarity 61.2%; Pred. No. 7e-11;
Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;

```

QY      8 CTATGCTGCTTCATTTACTTCATGCGATTTCTTCTTGGCAATGACCTCTTTGTTG 67
DB      38 CCAATGCTGCTTCATTTACTTCATGCGATTTCTTCTTGGCAATGACCTCTTTGTTA 97
QY      68 CTATGAGGTGAGCAAGCAAGAAATTTGC--TGTAAAGAGCTCACAACCTGTTAAAT 124
DB      98 CCAATGAGGTGAGCAAGCAAGAAATTTGC--TGTAAAGAGCTCACAACCTGTTAAAT 157
QY      125 GTTCTGATGACCTCTATGTCACAACTCTGTATGAGAGAGAAATATGAAATGTC 184
DB      158 GTTCTGATGACCTCTATGTCACAACTCTGTATGAGAGAGAAATATGAAATGTC 214
QY      185 ATTTGTTCACAATCTTAAGCAAGTCTTATGATGAGAGATGATGCTAAACCTCTG 244
DB      215 ATTTGTTCACAATCTTAAGCAAGTCTTATGATGAGAGATGATGCTAAACCTCTG 274
QY      245 CAACGAAT-----GCTGCTTG 263
DB      275 CAAGTAAAGTTAAAGCAACTTGGGTGAGAGCAAAACCTTAAGTAAAGTTGCTTG 334
QY      264 AAGAAGAGTCTCAAGCAAGTAAT-----TAAATTGATTAAGTAAAGT----- 311
DB      335 AAGAAGAGTATGATGAGATTAATTAAGTAAAGTAAATTAAGATTTGAGTCA 394
QY      312 --CAACAAATTAATTAAGTGTGCTTCTTAAGGTAACCTTAATATGTTG--T 366
DB      395 AAAAAACAAATTAATTAAGTGTGCTTCTTATTAAGGTAACCTTATGATGTGTT 454

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Oy 367 ATCTTGGTGTATAGTACCATTTGACACATTAATTAAGTTGTGACACATTCCTT 426
Db 455 AGATATGGCCCTATAGTACCATTTGACACATTAATTAAGTTGTGACACATTCCTT 513
Oy 427 CATTGATCTCTCAATTAAGTTGTGTTTAAGTAAGAGATCGTTTACGGCTTAA 485
Db 514 C-----TTATGATGATGATGTTTATGATGATAAATGATGACTGATGATCTTTAA 560

RESULT 6
ID AAT48813 standard; cDNA; 564 BP.
AC AAT48813;
XX
XX 14-MAR-1997 (first entry)
DE cDNA clone p2130 capable of directing ovary-tissue transcription.
XX
XX Ovary; fruit; colour; pigmentation; cotton; tomato; probe;
XX KM promoter; p2130; p27; transgenic plant; ds.
XX OS Lycopersicon esculentum cv. UC82B.
XX FH Key Location/Qualifiers
XX FT CDS 1..357
XX FT misc_RNA 447..564
XX FT /tag= a
XX FT /tag= b
XX FT /note= "bases 447-564 correspond to clone p27"
XX
XX W09640951-A2.
XX
XX 19-DEC-1996.
XX PD
XX PF 07-JUN-1996; 96WO-US09911.
XX PR 07-JUN-1995; 95US-0487087.
XX PA (CALJ ) CALGENE INC.
XX MCBrade K, Stalker DM;
XX PI
XX DR WPI; 1997-052341/05.
XX DR P-PSDB; AAW08364.
XX
XX DNA construct capable of directing ovary-tissue transcription in
XX PT plants - useful for modifying colour phenotype, in e.g. cotton
XX
XX Example 1; Fig 1; 75pp; English.
XX
XX A cDNA clone (AAT48813), designated p2130, comprises a tomato
XX transcriptional initiation region that is capable of directing
XX tissue, partic. early in fruit development, e.g. to modify colour
XX phenotype. It can also be used as a molecular probe. To obtain
XX p2130, a tomato pre-anthesis stage cDNA library was screened by
XX differential hybridisation. Clones p27 and p28 that hybridised
XX only to pre-anthesis probes were used to screen a second cDNA
XX library, yielding p2130 and p270 (see also AAT48814). A genomic
XX clone (AAT48816) was also isolated using p2130 as probe.
XX
XX Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;
SQ
Query Match 18.5%; Score 93.8; DB 18; Length 564;
Best Local Similarity 61.2%; Pred. No. 7e-11;
Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;
Oy 8 CTATGGCTCTTCATTTACTTCATGACATTTCTGTCTGCAATGACACTCTTTGTTG 67
Db 38 CATGGCTCTTCATTTACTTCATGACATTTTGTCTGTGCAATGATGCTCTTTGTTA 97

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Oy 68 CTTATGGGCTGCAAGGCAAGAAATTTGC---TGTAAGAGCTCACAAACTGTTAAT 124
Db 98 CCTATGAGGTAGAGAGCTCAGCAAAATTTTGCAAGCACCAGCCAAATTTTCCAGATTA 157
Oy 125 GTTCTAGTACCCCTCTATGTCAAAACCTGTGTGAGAGAGAAATATGAAATGCTC 184
Db 158 GTTTTATGACATCATCATGTAAGAAATATGTTT---CAAGAGAAATTTACTGGTGAC 214
Oy 185 ATTTGTTCAATCTTAAGCAAGTCTTATGATGAAAGAGATGTAATGCTAAACTCTG 244
Db 215 ATTTGAGCAAACTCCAAAGAGAGTGTCTATGACATAAGCCATGTATTTGCAAAATCT 274
Oy 245 CAACAGAAAT-----GCTTGCTTG 263
Db 275 CAAAGTAAGTTAAAGCAACTTGGGTGAGAGAGCAAAACTTAAGTAAGTGTGCTTG 334
Oy 264 AAGAGAGTCTCTCAGCAGTAAT-----TAAGTTGATTTAGGATTTAGCT----- 311
Db 335 AAGAGAGATTAATGATGAGATTAATTAAGTGAAGTAAATGAGATTTTGAAGTCA 394
Oy 312 --CACCAAAATTAATTAAGTGTGCTTTCTTAAGAGGTAAGTATATGTTG--T 366
Db 395 AAAAAACAAATTAATTAAGTGTGCTTTCTTAAGAGTGAAGTGTGTTGTT 454
Oy 367 ATCTTGGTGTATAGTACCATTTGACACATTAATTAAGTTGTGACACATTCCTT 426
Db 455 AGTATTTGGCTATAGTACCATTTGACACATTAATTAAGTTGTGACACATTCCTT 513
Oy 427 CATTGATCTCTCAATTAAGTTGTGTTTAAGTAAGAGATCGTTTACGGCTTAA 485
Db 514 C-----TTATGATGATGATGTTTATGATGATAAATGATGACTGATGATCTTTAA 560

RESULT 7
ID AB221970 standard; cDNA; 564 BP.
AC AB221970;
XX
XX 28-MAR-2003 (first entry)
DE Plasmid p2130 cDNA sequence p27.
XX KM Transcriptional factor; ovary tissue; gene; ss.
XX OS Unspecified.
XX
XX Key Location/Qualifiers
XX FT CDS 1..564
XX FT /tag= a
XX FT /partial
XX FT /product= "p2130 protein sequence"
XX FT /trans_except= (pos:355..357,aa:Xaa)
XX FT /trans_except= (pos:358..360,aa:Xaa)
XX FT /trans_except= (pos:376..378,aa:Xaa)
XX FT /trans_except= (pos:385..387,aa:Xaa)
XX FT /trans_except= (pos:436..438,aa:Xaa)
XX FT /trans_except= (pos:454..456,aa:Xaa)
XX FT /trans_except= (pos:478..480,aa:Xaa)
XX FT /trans_except= (pos:490..492,aa:Xaa)
XX FT /trans_except= (pos:541..543,aa:Xaa)
XX FT /note= "all Xaa's are encoded by stop codons"
XX
XX CN189856-A.
XX
XX 05-AUG-1998.
XX PD
XX PF 07-JUN-1996; 96CN-0195170.
XX PR 07-JUN-1995; 95US-0480087.
XX
XX (CALJ ) CALGENE INC.
XX

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DR WPI: 2002-733392/80.
 XX P-PSDB: ABP56255.

PT Use of transcriptional factors of ovary tissue -

XX Example 3, Fig 1A-B; 56pp; Chinese.

XX The present invention describes the use of transcriptional factors of
 CC ovary tissue. The present sequence represents a nucleotide sequence
 CC which is used in an example from the present invention.

XX Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;

Query Match 18.5%; Score 93.8; DB 24; Length 564;
 Best Local Similarity 61.2%; Pred. No. 7e-11;
 Matches 330; Conservative 0; Mismatches 132; Indels 77; Gaps 8;

```

QY 8 CTATGGCTGCTTCATTTACTTACTGATGCAATTTCTTGTTGGCAATGACACTCTTTGTTG 67
DB 38 CCAATGGCTGCTTCATTTACTTACTGATGCAATTTCTTGTTGGCAATGATGCTCTTTGTTA 97
QY 68 CTTATGGCTGCAAGCAAGCAAAATTTGC---TGTAAAGACTGCAAAACCTGTTAAAT 124
DB 98 CTTATGGCTGCAAGCAAGCAAAATTTGC---TGTAAAGACTGCAAAACCTGTTAAAT 157
QY 125 GTTCTAGTACCTCTATGTCACAAAACCTGATGAGAGAGAGAAATATGATGATGTC 184
DB 158 GTTTTATGAGCTCATGCTAGTAAATATGAT---CAAGAGAAATTTACTGTTGAGC 214
QY 185 ATTGTTTCAATCTTAAGCAAGCTTATGATGAGAGAGATGTAATGCTAAATCTCTCG 244
DB 215 ATTGTCACAAATCCCAAGAGAGATGCTATGACACTCAAGCCATGTAATTTGACAAATCT 274
QY 245 CAACAGAAAT-----GCTTGGCTTG 263
DB 275 CAGTGAAGTTTAAAGCACTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 334
QY 264 AAGAAGATCTTCAAGCAAGTAAAT-----TAAGTTGATTAAGCAATTAAGCT 311
DB 335 AAGAAGATTAAGTGAAGTAAATTAAGTGAAGTAAATTAAGTGAAGTGAAGTGAAGTGAAG 394
QY 312 --CACACAAATTAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 366
DB 395 AAAAAACAAATTAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 454
QY 367 ATTCTTGGTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 426
DB 455 AGATTGGCTTATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 513
QY 427 CATGTAATCTTCAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 485
DB 514 C-----TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 560

```

RESULT 8
 AAV70143 ID AAV70143 standard; cDNA to mRNA; 558 BP.
 XX AAV70143;
 AC
 XX 03-FEB-1999 (first entry)
 DT
 XX Nicotiana paniculata thionine gene NpTH1.
 DE Nicotiana paniculata thionine gene NpTH1.
 XX Nicotiana excelsior; Nicotiana paniculata; thionine; NpTH1; NpTH2;
 KM NpTH1; salt stress; resistance; ds.
 XX Nicotiana paniculata.
 OS
 XX Key Location/Qualifiers
 FH 48..368
 FT CDS /-tag= a
 FT XX

PN JP10295380-A.

XX 10-NOV-1998.

XX 23-APR-1997; 97JP-0120179.

XX 23-APR-1997; 97JP-0120179.

XX (NISB) JAPAN TOBACCO INC.

XX WPI: 1999-038278/04.

DR P-PSDB: AAW83133.

XX Thionine gene derived by salt stress - used to deliver improved salt

PS stress to plants

XX Claim 5; Page 5-6; 6pp; Japanese.

XX The present sequence represents a thionine gene from Nicotiana
 CC paniculata derived NpTH1. The thionine protein has an effect of
 CC improving the salt stress resistance of a plant. The gene can improve
 CC the salt stress resistance of a plant.

XX Sequence 558 BP; 175 A; 87 C; 112 G; 184 T; 0 other;

Query Match 18.2%; Score 92; DB 20; Length 558;
 Best Local Similarity 57.1%; Pred. No. 1.7e-10;
 Matches 275; Conservative 0; Mismatches 160; Indels 47; Gaps 4;

```

QY 1 AAGAAGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 60
DB 39 AAGAAGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 98
QY 61 TTGTTGCTTATGGGCTGCAAGCAAGCAAAATTTGCTGTAAGAGCTCAAAAACCTGTT 120
DB 99 TTGTTGCTTATGGGCTGCAAGCAAGCAAAATTTGCTGTAAGAGCTCAAAAACCTGTT 158
QY 121 AATGTTCTATGAGACCTCTATGTCAAAACCTGTAAGAGCAAGCAAAATTTGCTGTAAGAG 180
DB 159 GGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 218
QY 181 GGTCAATGTTTCAAACTTCAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 234
DB 219 GGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 278
QY 235 AAAAATCTGCAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 256
DB 279 AAGATGATCAAAACGAGCTGAAATTTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 338
QY 257 TTGCTGGAAGAGAGTTCCTCAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 314
DB 339 TTGCTGGAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 398
QY 315 ACAAATTAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 374
DB 399 GTCAACATTAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 458
QY 375 TGTATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 434
DB 459 CTTTATAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 517
QY 435 TT 436
DB 518 TT 519

```

RESULT 9
 AAV70142 ID AAV70142 standard; cDNA to mRNA; 566 BP.
 XX AAV70142;
 AC
 XX 03-FEB-1999 (first entry)
 DT

XX Nicotiana excelsior thionine gene NeTH12.
 DE Nicotiana excelsior; Nicotiana paniculata; thionine; NeTH1; NeTH12;
 XX Nicotiana excelsior; Nicotiana paniculata; thionine; NeTH1; NeTH12;
 KM NeTH1; salt stress; resistance; ds.
 XX Nicotiana excelsior.
 OS Nicotiana excelsior.
 XX Key Location/Qualifiers
 FT CDS 33..350
 FT /*tag= a
 XX JPI0295380-A.
 XX 10-NOV-1998.
 XX 23-APR-1997; 97UP-0120179.
 XX 23-APR-1997; 97UP-0120179.
 XX 23-APR-1997; 97UP-0120179.
 XX (NISR) JAPAN TOBACCO INC.
 XX WPI: 1999-038278/04.
 DR P-PSDB; AAM83132.
 XX Thionine gene derived by salt stress - used to deliver improved salt
 PT stress to plants
 XX Claim 3; Page 5; 6pp; Japanese.
 XX The present sequence represents a thionine gene from Nicotiana excelsior
 CC derived NeTH12. The thionine protein has an effect of improving the salt
 CC stress resistance of a plant. The gene can improve the salt stress
 CC resistance of a plant.
 XX Sequence 566 BP; 178 A; 94 C; 108 G; 186 T; 0 other;
 SQ

Query Match 18.2%; Score 92; DB 20; Length 566;
 Best Local Similarity 65.8%; Pred. No. 1.7e-10;
 Matches 150; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

QY 1 AAGAGACTATGAGCTGCTTCATTTACTTCATGAGATTCTTGTCTTGGAATGACATC 60
 DB 24 AAGAGACTATGAGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 83
 QY 61 TTGTGCTTATGAGGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 120
 DB 84 TTGTGCTTATGAGGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 143
 QY 121 AATGCTTATGAGCTGCTGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 180
 DB 144 AATGCTTATGAGCTGCTGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 200
 QY 181 GGCATGCTTATGAGCTGCTGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 228
 DB 201 GGCATGCTTATGAGCTGCTGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 248

RESULT 10
 AAV70141
 ID AAV70141 standard; cDNA to mRNA; 456 BP.
 XX AAV70141;
 XX 03-FEB-1999 (first entry)
 XX Nicotiana excelsior thionine gene NeTH11.
 DE Nicotiana excelsior; Nicotiana paniculata; thionine; NeTH1; NeTH12;
 XX Nicotiana excelsior; Nicotiana paniculata; thionine; NeTH1; NeTH12;
 KM NeTH1; salt stress; resistance; ds.
 XX Nicotiana excelsior.
 OS Nicotiana excelsior.

FH Key Location/Qualifiers
 FT CDS 1..240
 FT /*tag= a
 XX JPI0295380-A.
 XX 10-NOV-1998.
 XX 23-APR-1997; 97UP-0120179.
 XX 23-APR-1997; 97UP-0120179.
 XX 23-APR-1997; 97UP-0120179.
 XX (NISR) JAPAN TOBACCO INC.
 XX WPI: 1999-038278/04.
 DR P-PSDB; AAM83131.
 XX Thionine gene derived by salt stress - used to deliver improved salt
 PT stress to plants
 XX Claim 1; Page 4; 6pp; Japanese.
 XX The present sequence represents a thionine gene from Nicotiana excelsior
 CC derived NeTH11. The thionine protein has an effect of improving the salt
 CC stress resistance of a plant. The gene can improve the salt stress
 CC resistance of a plant.
 XX Sequence 456 BP; 149 A; 73 C; 88 G; 146 T; 0 other;
 SQ

Query Match 13.3%; Score 67.2; DB 20; Length 456;
 Best Local Similarity 56.2%; Pred. No. 2.9e-05;
 Matches 244; Conservative 0; Mismatches 158; Indels 32; Gaps 5;

QY 58 CTCTTTGCTTATGAGGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 117
 DB 1 CTCTTTGCTTATGAGGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 54
 QY 118 GTTAATGCTTATGAGGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 177
 DB 55 GACTATGCTTATGAGGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 111
 QY 178 GATGCTTATGAGGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 234
 DB 112 GATGCTTATGAGGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 171
 QY 235 AAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 277
 DB 172 GAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 231
 QY 278 AAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 334
 DB 232 GATGCTTATGAGGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 291
 QY 335 GCTTTCTTAAAGGCTGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 394
 DB 292 ACCTTTCTTAAAGGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 351
 QY 395 CATTAATTAAGGCTGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 454
 DB 352 CACTTTAAATTAAGGCTGCTGCTGCTGCTGCTTCATGAGATTCTTGTCTTGGAATGACATC 411
 QY 455 TTAATGAAGAAGA 468
 DB 412 TACTTTAATGAAGA 425

RESULT 11
 AAT31824
 ID AAT31824 standard; cDNA; 3528 BP.
 XX AAT31824;
 XX 25-MAR-2003 (updated)

DT	14-SEP-1996 (first entry)
XX	Tomato pz130 genomic clone Calgene Lambda 140.
DE	Ovary; ovule; fruit; tomato; cotton; melanin; vector;
XX	transgenic plant; ss.
KM	
XX	
OS	Lycopersicon esculentum cv. UC82B.
XX	
XX	Key Location/Qualifiers
PH	
FT	misc_difference 586
FT	/note= "base n at position 586 is unidentified"
FT	
FT	misc_difference 590
FT	/note= "base n at position 590 is not identified"
FT	/tag= b
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FT	misc_difference 591
FT	/tag= c
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FT	misc_difference 663
FT	/tag= d
FT	/note= "base n at position 663 is not identified"
FT	misc_difference 667
FT	/tag= e
FT	/note= "base n at position 667 is not identified"
FT	misc_difference 769
FT	/tag= f
FT	/note= "base n at position 769 is not identified"
FT	misc_difference 2483
FT	/tag= g
FT	/note= "base 2483 is given as s in the specification"
FT	misc_difference 2485
FT	/tag= h
FT	/note= "base 2485 is given as s in the specification"
FT	
FT	exon
FT	2567..2701
FT	/tag= i
FT	2702..2921
FT	/tag= j
FT	2922..3528
FT	/tag= k
XX	
XX	US5530185-A.
PN	
XX	
PD	25-JUN-1996.
XX	
PF	29-DEC-1992. 92US-0998158.
XX	
XX	29-DEC-1992. 92US-0998158.
PR	19-JUL-1989. 89US-0382518.
PR	17-JUL-1990. 90US-0554195.
XX	
PA	(CALJ) CALGENE INC.
PI	
PI	Martineau BM, Reilley AA, Stalker DM.
DR	WPI; 1996-308822/31.
DR	P-PSDB; AAR97559.
XX	
PT	DNA construct for expressing melanin synthesis gene in plant ovule
PT	cells - contains promoter from the tomato pz130 gene, also binary
PT	vector and transgenic plants, esp. cotton, contg. construct
PS	Example 5; Fig 2A-C; 25pb; English.
XX	
XX	The tomato pz130 genomic clone (AAT31824) was isolated from a genomic
CC	library using a pz130 cDNA clone (AAT31823) as probe. The pz130
CC	transcriptional initiation region is considered to be ovary-specific.
CC	It can be utilized in DNA constructs for the expression of
CC	heterologous genes, partic. in early fruit development, and esp. for
CC	expression of a melanin synthesis gene in transgenic cotton. The
CC	native function of the pz130 gene product (AAR97559) is unknown.
CC	

```

CC (Updated on 25-MAR-2003 to correct PF field.)
XX
S0 Sequence 3528 BP; 1191 A; 529 C; 518 G; 1282 T; 8 other;
Query Match 12.4%; Score 62.6; DB 17; Length 3528;
Best Local Similarity 64.8%; Fred. No. 0.00034;
Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3
OY 262 TGAGAGAGAGTCCCAAGCAGAGTAAATAGTTGATTAGTATGATGTCACACAAAT 321
DB 3165 TGATGAGATTAATTAATGAGGTAAATAGGATTTTGAAGTCCAAAACAAAT 3222
OY 322 TAAATTAAGTGTGCTTTCTTAAAGGTAAGTAAAGTGTATC---TTGGTGA 378
DB 3225 TAAATTAAGTGTGCTTTCTTAAAGGTAAGTGTGATGATGTGTAGTATGGCCTA 3284
OY 379 TAGTACCATTTGCACACATTAATTAAGTGTGACACATCAATCCCTCATGTATCTCT 438
DB 3285 TAGTACCATTTGCACACATTAATTAAGTGTGACACATCAATCCCTCATGTATCTCT 3332
OY 439 ATTAAGTTGTGCTTTTAAATGAAGAAAGATTCGTTAAGGCTTAAAT 485
DB 3333 -TTATGTATGTAATGTTTAAATGAAGAAATGATCAGTACATCTTAA 3378

RESULT 12
AAT48816
ID AAT48816 standard; cDNA; 3528 BP.
XX
AC AAT48816;
XX
DT 14-MAR-1997 (first entry)
XX
DE Calgene Lambda 140 genomic clone.
XX
KW Ovary; fruit; colour; pigmentation; cotton; tomato; probe;
KW promoter; pZ130; pZ7; transgenic plant; ss.
XX
OS Lycopersicon esculentum cv. UC82B.
XX
FH Key Location/Qualifiers
FT exon /*tag= a
FT intron 2702..2921
FT exon /*tag= b
FT exon 2922..3528
FT misc_RNA /*tag= c
FT misc_RNA 2599..2701
FT misc_RNA /*tag= d
FT misc_RNA /*note= "5' end of pZ130 gene"
FT misc_RNA 2922..3382
FT misc_RNA /*tag= e
FT misc_RNA /*note= "3' end of pZ130 gene"
XX
EN NO9640951-A2.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US09911.
XX
PR 07-JUN-1995; 95US-0487087.
XX
PA (CALJ ) CALGENE INC.
XX
PI McBrade K, Stalker DM;
XX
WP; 1997-052341/05.
XX
DR DNA construct capable of directing ovary-tissue transcription in
PT plants- useful for modifying colour phenotype, in e.g. cotton
XX
SS Example 7; Fig 2; 75pp; English.
XX

```


SQ Sequence 4383 BP; 1539 A; 620 C; 610 G; 1606 T; 8 other;

Query Match 12.4%; Score 62.6; DB 12; Length 4383;
 Best Local Similarity 64.8%; Pred. No. 0.00035;
 Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;

QY 262 TGAAGAAGAGTTCCTCAAGCAGTAATTAGTTGATTATGATTTAGTGTACACAAAT 321
 DB 3165 TGATGAGTAATTAATTAAGTGAAGTTAAATAGATTGAGTCAAAAAACAAAT 3224

OY 322 TAAATTAAGTGTGCTTCTTAAGAGGTAACTTAATATGTTGTTATTC---TTGGTGA 378
 DB 3225 TAAATAAGTGTGCTTCTTCTTAATGAGGTAGCTTGATGTTGTGTTAGTATGGCCCA 3284

OY 379 TAGTACCATTTGACACATTAATAATTAAAGTTGTGACATCAATCCTTCATGTTCT 438
 DB 3285 TAGTACCATTTGACACATTAATAATTAAAGTTGTGACATCAATCCTTCATGTTCT 3332

OY 439 ATTAAGTTGTGTTTAAATGAAGAAGATCGTTACGGCTAATA 485
 DB 3333 -TTATGTATGTATGTTTAAATGAAGAAGATCGATCACTACATCTTTAA 3378

SQ Sequence 4383 BP; 1539 A; 620 C; 610 G; 1606 T; 8 other;

Query Match 12.4%; Score 62.6; DB 12; Length 4383;
 Best Local Similarity 64.8%; Pred. No. 0.00035;
 Matches 147; Conservative 0; Mismatches 64; Indels 16; Gaps 3;

QY 262 TGAAGAAGAGTTCCTCAAGCAGTAATTAGTTGATTATGATTTAGTGTACACAAAT 321
 DB 3165 TGATGAGTAATTAATTAAGTGAAGTTAAATAGATTGAGTCAAAAAACAAAT 3224

OY 322 TAAATTAAGTGTGCTTCTTAAAGAGGTAACTTAATATGTTGTTATTC---TTGGTGA 378
 DB 3225 TAAATAAGTGTGCTTCTTCTTAATGAGGTAGCTTGATGTTGTGTTAGTATGGCCCA 3284

OY 379 TAGTACCATTTGACACATTAATAATTAAAGTTGTGACATCAATCCTTCATGTTCT 438
 DB 3285 TAGTACCATTTGACACATTAATAATTAAAGTTGTGACATCAATCCTTCATGTTCT 3332

OY 439 ATTAAGTTGTGTTTAAATGAAGAAGATCGTTACGGCTAATA 485
 DB 3333 -TTATGTATGTATGTTTAAATGAAGAAGATCGATCACTACATCTTTAA 3378

Search completed: August 23, 2003, 05:57:20
 Job time : 217 secs

RESULT 15
 AAQ10319 standard; cDNA; 4383 BP.

AAQ10319;
 AC 25-MAR-2003 (updated)
 XX 04-APR-1991 (first entry)
 DT
 XX Calgene lambda 140 genomic clone.
 XX
 XX p2130; cytokinin; ds.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT misc_RNA 2567..3382
 FT /*tag= a
 FT /note= "Sequence homologous to p2130 transcript"
 FT misc_RNA 2599..3382
 FT /*tag= b
 FT /note= "Sequence homologous to p2130 CDS"
 FT misc_RNA 2702..2921
 FT /*tag= C
 FT /note= "Sequence homologous to p2130 intron"

EP409628-A.
 XX
 XX 23-JAN-1991.
 XX
 XX 19-JUL-1990; 90BP-0307925.
 XX
 XX 19-JUL-1989; 89US-0382802.
 XX
 XX (CALJ) CALGENE, INC.
 XX
 XX Houck CM, Pear JR, Martineau B, Hiatt W;
 XX
 XX WPI; 1991-024190/04.
 XX
 XX Modulating endogenous cytokinin levels - regulatory regions are
 XX transformed into plant cells e.g. fruit to modify pheno-type
 XX
 XX Disclosure; Fig 3; 39pp; English.
 XX
 XX The sequence encodes an enzyme in the cytokinin biosynthetic pathway,
 XX derived from z130, and useful in modulating a transformed plant's
 XX phenotype eg. fruit maturation, ripening etc.
 XX (updated on 25-MAR-2003 to correct PA field.)
 XX

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2003, 02:54:57 ; Search time 1998 Seconds
(without alignments)
10360.496 Million cell updates/sec

Title: US-09-854-562-1

Sequence: 1 aaagagactatgctcgttc.....aaaaaaaaaaaaaaaaaaaaa 506

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba: *
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6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	504.4	99.7	506	8	AF112443
2	494.8	97.8	548	8	AF112869
3	242.8	48.0	559	8	AF128239
4	106.2	21.0	601	8	AF509566
5	102.8	20.3	596	8	SLU20591
6	96.6	19.1	589	8	SESTRNA
7	92	18.2	549	8	AB005250
8	92	18.2	558	8	AB005265
9	67.2	13.3	448	8	AB005265
10	56	11.1	110000	2	PFMAL7P1_05
11	53.6	10.6	331039	3	AC116988
12	52.8	10.4	51729	9	AC118276
13	52.6	10.4	254050	3	PEA929358
14	52.2	10.3	110000	3	AC116984_3
15	51.6	10.2	86826	3	PFMAL3P5
16	51.4	10.2	3764	9	BC024739
17	51.2	10.1	110000	3	AC116305_0
18	51.2	10.1	196490	2	AC005507
19	51	10.1	30849	3	AC117082
20	51	10.1	39575	3	AC116925
21	50.6	10.0	36148	3	AC116100
22	50.6	10.0	80804	2	AC128660
23	50.2	9.9	602	8	AF507976
24	50	9.9	1999	9	BC020684
25	49.8	9.8	7669	6	AX345531
26	49.8	9.8	162539	5	AL954372
27	49.8	9.8	293431	2	PFMAL13P4
28	49.6	9.8	114426	2	AC004710
29	49.6	9.8	250421	3	AE014849
30	49.6	9.8	254733	3	AC117075
31	49.4	9.8	9751	3	AF465309
32	49.4	9.8	110000	2	PFMAL13_01
33	49.4	9.8	125958	3	AC115592
34	49.4	9.8	192881	2	PFMAL13P1
35	49.4	9.8	250663	3	AE014826
36	49.4	9.8	260929	3	AE014852
37	49.4	9.8	310779	2	AC005140
38	49	9.7	2787	3	PESTARP
39	49	9.7	110000	2	PFMAL7P1_00
40	48.8	9.6	310	3	AF118005
41	48.8	9.6	1646	10	BC004087
42	48.8	9.6	3873	6	AX458573
43	48.8	9.6	41399	3	AC116984_5
44	48.8	9.6	61052	2	AC123513
45	48.8	9.6	110000	3	AC116984_4

ALIGNMENTS

RESULT 1
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LOCUS AF112443 506 bp mRNA linear PLN 10-DEC-1999
DEFINITION Capsicum annuum thionin-like protein (pephti) mRNA, complete cds.
ACCESSION AF112443
VERSION AF112443.1 GI:6552501
KEYWORDS Capsicum annuum
SOURCE Capsicum annuum
ORGANISM Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Lamiales; Solanales; Solanaceae; Capsicum.
REFERENCE Oh, B.J., Ko, M.K., Kostenyuk, I., Shin, B. and Kim, K.S.
AUTHORS 1 (bases 1 to 506)
TITLE Coexpression of a defensin gene and a thionin-like via different

signal transduction pathways in pepper and *Colletotrichum*
gloeosporioides interactions
 Plant Mol. Biol. 41 (3), 313-319 (1999)
 JOURNAL
 MEDLINE
 2004969
 PUBMED
 10598099
 REFERENCE
 2 (bases 1 to 506)
 AUTHORS
 Oh, B.J., Ko, M.K., Koestenyuk, I.A., Shin, B.C. and Kim, K.S.
 TITLE
 Direct Submision
 Submitted (09-DEC-1998) Kumbo Life and Environmental Science
 Laboratory, Kumbo Petrochemical Co., LTD., 1 Oryong-dong, Puk-gu,
 Kangju 500-712, Korea
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 Best Local Similarity 99.8%; Pred. No. 1.8e-96;
 Matches 505; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAAGAGACTAGGCTGCTGCATTTACTTCAATGAGCATTTCTTGCTTGCAATGACATC 60
 DB 1 AAAGAGACTAGGCTGCTGCATTTACTTCAATGAGCATTTCTTGCTTGCAATGACATC 60
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 QY 481 TAAAAAAGAAAAA 506
 DB 481 TAAAAAAGAAAAA 506
 RESULT 2
 AF112869 548 bp mRNA linear PLN 19-DEC-1999

DEFINITION Capsicum annuum gamma-thionin 1 precursor (thionin) mRNA, complete cds
 ACCESSION AF112869
 VERSION AF112869.1 GI:6601330
 KEYWORDS
 SOURCE
 ORGANISM
 Capsicum annuum
 Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamiales; Solanales; Solanaceae; Capsicum.
 REFERENCE
 1 (bases 1 to 548)
 AUTHORS
 Hwang, B.K., Lee, S.C., Kim, Y.J. and Hong, J.K.
 TITLE
 Molecular cloning and pathogen-induced expression of a thionin gene
 in pepper plants
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 548)
 AUTHORS
 Hwang, B.K., Lee, S.C., Kim, Y.J. and Hong, J.K.
 TITLE
 Direct Submission
 Submitted (10-DEC-1998) Dept. of Agricultural Biology, Korea
 University, Anam-dong, Sungbuk-gu, Seoul 136-701, Korea
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 sig_peptide
 52..114
 /gene="thionin1"
 115..303
 /gene="thionin1"
 /product="gamma-thionin 1"
 366..371
 /gene="thionin1"
 BASE COUNT 186 a 76 c 107 g 179 t
 ORIGIN
 Query Match 97.8%; Score 494.8; DB 8; Length 548;
 Best Local Similarity 98.6%; Pred. No. 1.9e-94;
 Matches 499; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 AAAGAGACTAGGCTGCTGCATTTACTTCAATGAGCATTTCTTGCTTGCAATGACATC 60
 DB 43 AAAGAGACTAGGCTGCTGCATTTACTTCAATGAGCATTTCTTGCTTGCAATGACATC 102
 QY 61 TTTGTTGCTTAGGGGTGCAAGGCAAGAAATTTGCTGTAAAGGCTCACAAACCTGTT 120
 DB 103 TTTGTTGCTTAGGGGTGCAAGGCAAGAAATTTGCTGTAAAGGCTCACAAACCTGTT 162
 QY 121 AAATGTTAGTAGACCTCTATGTCAAAACCTGTATGAGAGAGAAATATGAAGAT 180
 DB 163 AAATGTTAGTAGACCTCTATGTCAAAACCTGTATGAGAGAGAAATATGAAGAT 222
 QY 181 GGTATTGTTTCAACATCTTAAGCAAGGCTTATGACATGAAGATATGATAACT 240
 DB 223 GGTATTGTTTCAACATCTTAAGCAAGGCTTATGACATGAAGATATGATAACT 282
 QY 241 CTGCAACAGAAATGCTGCTTGAAGAGATTCCTCAGACATTAATTAAATTGATTAT 300
 DB 283 CTGCAACAGAAATGCTGCTTGAAGAGATTCCTCAGACATTAATTAAATTGATTAT 342
 QY 301 GGAATTAGTGCACAAATTAATAAGTGGCTTCTTAAAGGTAATCTTATA 360

Db	343	CGATTAGTGCACACAATAATTAATAAGTGTCCTTTCTTAAGAAGGTAACTTATTA	402
Oy	361	TGTTGATTTCTTGCTGTATATAGCACTTGGACATTAATAATTAAAGTTGTACACATCA	420
Db	403	TGTTGATTTCTTGAGTAGTAGAGCACTTGGACATTAATAATTAAAGTTGTACACATCA	462
Oy	421	ATCCTTCATGATATCTTCTAATTAAAGTTGTGTGTTTATATGAAGAAGATCGTTTACGGTC	480
Db	463	ATCCTTCATGATATCTTCTAATTAAAGTTGTGTGTTTATATGAAGAAGATCGTTTACGGTC	522
Oy	481	TT	506
Db	523	TATATGTAAAAAAAAAAAAAAAAAAAAAAA	548
<hr/>			
RESULT 3	AFI28239	559 bp	mRNA linear
LOCUS	AFI28239		PIN 06-JUL-1999
DEFINITION	Capsicum chinense putative gamma-thionin precursor, mRNA, complete cds.		
ACCESSION	AFI28239		
VERSION	AFI28239.1	GI:4457222	
KEYWORDS			
SOURCE			
ORGANISM	Capsicum chinense Capsicum chinense Eubryotia; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; Lamiales; Solanales; Solanaceae; Capsicum. 1 (bases 1 to 559) Aluru,M., Curry,J., and O'Connell,M.A. Nucleotide sequence of a defensin or gamma-thionin-like gene (Accession No. AFI28239) from habanero chile (PGR 99-070) Plant Physiol. 120 (2), 633 (1999) 2 (bases 1 to 559) Curry,J., Aluru,M. and O'Connell,M.A. Direct Submission Submitted (12-FEB-1999) Agronomy and Horticulture, New Mexico State University, P.O. Box 30003, MSC 30, Las Cruces, NM 88003, USA Location/Qualifiers 1..559 .organism="Capsicum chinense" /mol_type="mRNA" /cultivar="habanero" /db_xref="taxon:80379" 39..362 /note="defensin" /codon_start=1 /product="putative gamma-thionin precursor" /protein_id="AAD21200.1" /db_xref="GI:4457223" translation="MARSIYMAFLVLAATLVANGVGONNI CKTTSKHPGLCPAL SKRKAKIEDFEDEGHCKSKQRKCDLCTKNQVPDNLINDVTILVDATLEADLE ELIGL"		
FEATURES	source		
JOURNAL			
AUTHORS			
TITLE			
REFERENCE			
JOURL			
CDS			
BASE COUNT	181 a	84 c	104 g 190 t .
ORIGIN			
Query Match	48.0%;	Score 242.8;	DB 8; Length 559;
Best Local Similarity	74.6%;	Pred. No. 2.7e-41;	
Matches 397;	Conservative 0;	Mismatches 77;	Indels 58; Gaps 5;
Oy	1	AAAGAGCATATGCGTCGTCGTCATTTACTTANTGCGATTTCTGTGCTTGGCAATGACATC	60
Db	30	AAAGAGCATATGCGTCGTCGTCATTTACTTANTGCGATTTCTGTGCTTGGCAATGACATC	89
Oy	61	TTTGTGCTTATGGGGGTGCAGGCAAGGAAATTGCTGTAAAGAGCTCACAAAACCTGTT	120
Db	90	TTTGTGCTTATGGGGGTGCAGGCAAGGCAAAATAACAATTGCCAAACACACAAACATTTT	149
Oy	121	AA-----ATGCTCTAGTACCCCTCAATGATCAAAGCTGATAGGAGAGAGAAATAT	174
Db	150	AAAGATTAATGTTTTCGCGACCTCTAAATAGTAGAAAAGTTTGATATCCAGAGAGATTAATTT	209
Oy	175	GAAATGATGTCATTTGTTCAACATCTTAAGCAAGTCTTAATGATGAAGAATGT-----	228

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MDN"
 mat_peptide 136..276
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 /product="flower-specific defensin"
 BASE COUNT 192 a 95 c 115 g 199 t
 ORIGIN

Query Match 21.0%; Score 106.2; DB 8; Length 601;
 Best Local Similarity 57.8%; Pred. No. 1.7e-12;
 Matches 322; Conservative 0; Mismatches 173; Indels 62; Gaps 5;

QY 1 AAGAGACATAGGCTGCTTCCATTTACTATGCGATTTCTGCTGGCAATGACACG 60
 DB 52 AAGAGACATAGGCTGCTTCCATTTACTATGCGATTTCTGCTGGCAATGACACG 111
 QY 61 TTGTTGCTATGCGGTGCGACGCAAGAAATTCCTGTAAAGACTCACAAAACCTGTT 120
 DB 112 TTGTTGCTATGCGGTGCGACGCAAGAAATTCCTGTAAAGACTCACAAAACCTGTT 171
 QY 121 AATGTTCTAGAGACCTCTATGTCAAAACCTCTATGAGAGAGAAATGAAAGAT 180
 DB 172 ATATGATTCACCAACACACATGACGAAAGCTGTGTAT--CACTGAAATTTACTGAT 228
 QY 181 GGTGATTTGTTTCAATCTCTAAGCAAGTCTTATGATGAGATGT-----228
 DB 229 GGTGATTTGTTTCAATCTCTAAGCAAGTCTTATGATGAGATGT-----228
 QY 229 -----AATGCTAAACTCTCGCAAGAA 252
 DB 289 AAGATGATTAACAGAGAGCTGAAATTTGGCTGAGGAGCAAAACCTTGGCTGAGCT 348
 QY 253 TTGCTTGCTTGA---AGAAAGTTCCTCAAGCAGTAAATTAATTAATTAATTAAT 309
 DB 349 TTGCTTGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 408
 QY 310 GTACACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 369
 DB 409 ATACACATTAATTAAT---TTTACCTTTCTTAAGTGTAGCTTAATTTGTGTTTA 464
 QY 370 CTGCTGTATAGTACCATTTGACACATTAATTAATTAATTAATTAATTAATTAAT 429
 DB 465 ATGGCTTTTATAGTACCTTTTATTAACCTTAATAAAGTGTGACCTTCAATCTTGTG 524
 QY 430 GTATCTTTATTAAG---TTTGTGTGTTTAAAGAAAGATCGTTGCGTCAAAA 485
 DB 525 CAATCTTGACCTAAGTTTATTTGTGTACTTTAATGAAGAAATGACCTTCTATGATCTTTGG 584
 QY 486 AAAAAAAAAAAAAA 502
 DB 585 TTAATAAAAAAAAAAAAA 601

RESULT 5
 SLID0591 596 bp mRNA linear PLN 04-NOV-1995
 LOCUS Solanum lycopersicum flower-specific gamma-thionin-like
 DEFINITION protein/acidic protein precursor, mRNA, complete cds.
 U20591
 U20591.1 GI:924623

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Lycopersicon esculentum (tomato)
 Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 596)
 MILLIGAN,S.B. and GAESEER,C.S.
 TITLE Nature and regulation of pistil-expressed genes in tomato
 JOURNAL Plant Mol. Biol. 28 (4), 691-711 (1995)
 MEDLINE 95375233
 PUBMED 7647301
 REFERENCE 2 (bases 1 to 596)
 AUTHORS Milligan,S.B.

TITLE Direct Submission
 JOURNAL Submitted (02-FEB-1995) Stephen B. Milligan, Molecular and Cellular
 Biology, University of California at Davis, Davis, CA 95616, USA
 FEATURES
 source
 1..596
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
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 /db_xref="taxon:4081"
 /clone="TTP3"
 /tissue_type="pistil"
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 /dev_stage="immature"
 1..56
 57..374
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 protein/acidic protein precursor"
 /protein_id="AA0496.1"
 /db_xref="GI:924624"
 /translation="MARSIPEPMAPIVLAAMLPVYVEVAQOICAKPSQPRGICMDS
 SKRKCINKEFTGCHSRDLQRKCLTRPCVFDKISEVATLGEAKTLSEVLEEEI
 MEE"

QY 8 CTATGCGCTGCTGCTTCTTCAATGCGATTTCTGCTGGCAATGACACCTTTGTTG 67
 DB 55 CCAATGCTGCTGCTTCTTCAATGCGATTTCTGCTGGCAATGACACCTTTGTTG 114
 QY 68 CTATGCGCTGCTGCTTCTTCAATGCGATTTCTGCTGGCAATGACACCTTTGTTG 124
 DB 115 CCAATGCTGCTGCTTCTTCAATGCGATTTCTGCTGGCAATGACACCTTTGTTG 174
 QY 125 GTTCTAGTACCTCTATGTCAAAACCTCTATGAGAGAGAAATTAATTAATTAAT 184
 DB 175 GTTCTAGTACCTCTATGTCAAAACCTCTATGAGAGAGAAATTAATTAATTAAT 231
 QY 185 ATGTTTCAATCTTAAGAGTCTTATGACAGAGATTAATTAATTAATTAATTAAT 244
 DB 232 ATGTTTCAATCTTAAGAGTCTTATGACAGAGATTAATTAATTAATTAATTAAT 291
 QY 245 CAACAGATTT-----GTTGCTTG 263
 DB 292 CAAGTGAATTAACCACTTGGGTGAGAGAAACCTAATGAAGTTGTTGCT 351
 QY 264 AAGAGAGTCTCTCAAGAGATTAAT---TAAGTTGATTAATGAATTAAGTTG 311
 DB 352 AAGAGAGTCTCTCAAGAGATTAAT---TAAGTTGATTAATGAATTAAGTTG 411
 QY 312 ---CACACAAATTAATTAAGTCTCTCTTCTTAAGAGGTTAATTAATTAATTTG 365
 DB 412 AAAAAAAAAAATTAATTAAGTCTCTCTTCTTATTAAGAGGTTAATTAATTTG 471
 QY 366 TATTTGCTGATAGTACCATTTGACACATTAATTAATTAATTAATTAATTAAT 425
 DB 472 TATTTGCTGATAGTACCATTTGACACATTAATTAATTAATTAATTAATTAAT 530
 QY 426 TATGATCTCTATTAAGTTGTTGTTTAATGAAGAGATCTTACGCTTAATA 485
 DB 531 CC-----TTATGATAGTATTTTAAATGAAGATGACATGACATCTTTAA 578
 QY 486 AAAAAAAAAAAAAA 503

Query Match 20.3%; Score 102.8; DB 8; Length 596;
 Best Local Similarity 61.5%; Pred. No. 9e-12;
 Matches 343; Conservative 0; Mismatches 137; Indels 78; Gaps 8;

BASE COUNT 204 a 82 c 107 g 203 t
 ORIGIN

3'UTR
 sig_peptide 57..134
 mat_peptide 135..275
 /product="gamma-thionin-like protein"
 /product="acidic protein"
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 3'UTR 375..596

Db 579 TTTTATTAATAAAAAAAAAA 596

RESULT 6
SFASTRNA
LOCUS Solanaceae mRNA for flower-specific thionin. 589 bp mRNA linear PLN 03-DEC-1993
DEFINITION Z11748 S41631
VERSION Z11748.1 GI:21212
KEYWORDS Thionin.
SOURCE Solanaceae
ORGANISM Solanaceae
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales.
REFERENCE 1 (bases 1 to 589)
Gu, Q., Kawata, E.E., Morse, M.J., Wu, H.M. and Cheung, A.Y.
A flower-specific cDNA encoding a novel thionin in tobacco
JOURNAL Mol. Gen. Genet. 234 (1), 89-96 (1992)
MEDLINE 92357021
PUBMED 1495489
REFERENCE 2 (bases 1 to 589)
Gu, Q.
Direct Submission
Submitted (25-FEB-1992) Qing Gu, Department of Biology, Yale University, 165 Prospect St, New Haven, CT, 06511, USA
JOURNAL Location/Qualifiers
FEATURES
source
1. 589
/organism="Solanaceae"
/mol_type="mRNA"
/db_xref="taxon:4070"
/clone="49A"
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/dev_stage="flowering"
49. 366
/codon_start=1
/product="flower-specific thionin"
/protein_id="CAA77806.1"
/db_xref="GI:21213"
/translation="MARSLCFMAFPAVLAMMFLPAYEVOAKSTKASNTFPGICITKPK
CRKACISEKFTDGHCSKILRRCLCTKPCVDEKMIKTGAETLVEAKTLAALLLEEI
MN"

BASE COUNT 184 a 97 c 114 g 194 t

ORIGIN

Query Match 19.1%; Score 96.6; DB 8; Length 589;
Best Local Similarity 56.7%; Pred. No. 1.8e-10;
Matches 316; Conservative 0; Mismatches 179; Indels 62; Gaps 5;

QY 1 AAAGAGCTATGCTGCTGCTTCATTACTTCATGCGATTTCTTGTCTTGGCAATGACATC 60
DB 40 AAAGAGCTATGCTGCTGCTTCATTACTTCATGCGATTTCTTGTCTTGGCAATGACATC 99
QY 61 TTGTTGCTTATGGGTGCAAGGCAAGAAATTTCTGTAAAGCTCACAAACCTGTT 120
DB 100 TTGTTGCTTATGGGTGCAAGGCAAGAAATTTCTGTAAAGCTCACAAACCTGTT 159
QY 121 AAATGTTCTAGTACCTCTATGTCAAAACCTGTATGAGAGAGAAATATGAAGAT 180
DB 160 ATATGCTTATCCAAACCATGACAGAAAGCTGTAT--CACTGAGAAATTTACTGAT 216
QY 181 GGTCTATGTTTCTCATCTCTAAGCAAGGCTTATGCAAGAGATGTT----- 228
DB 217 GGTCTATGTTTCTCATCTCTAAGCAAGGCTTATGCAAGAGATGTT----- 276
QY 229 -----AATGCTAAACCTCTGCAAGAA 252
DB 277 AAGATGATAAAACAGAGAGCTAAACTTTGTTGAGAAACAAACCTTTGGCTGAGCT 336
QY 253 TTGTTGCTTGA--AGAAGATTCCTCAAGAGAAATTAAGTTGATTGATTAAGT 309

Db 337 TTGCTTGAAAGAGATATGATTAATTAAGATTAGACATTGAAAGAACTTAGACACAGT 396
QY 310 GTGACACAAATTAATAAGTGTGCTTCTTAAAGGGTAACTATATGTTGAT 369
DB 397 GTGACACATTAATAAGT-----TGCTACCTTCTTAAAGGTAGTAAAGTTGTTTAA 452
QY 370 CTGGGTATGATGACATTTGACACATTAATTAAGTGTGACACATCAATCTTCAT 429
DB 453 ATTGCTTTATGATGACCTTTGTTTACCTTAAATTAAGTGTGACATTCATCTTTG 512
QY 430 GATGCTTATTAAGTTT---GTGCTTTAATGAAAGATCGTTTACGCTTAAA 485
DB 513 CATCTTGACACTAAGTTTATGCTGTTATTAATGAAATGACCTTATGCTTTGT 572
QY 486 AAAAAAAAAAAAAA 502
DB 573 TTTATTTGAAAAAAAAA 589

RESULT 7
LOCUS AB005250
DEFINITION Nicotiana paniculata mRNA for gamma-thionin, complete cds.
ACCESSION AB005250
VERSION AB005250.1 GI:2251080
KEYWORDS gamma-thionin.
SOURCE Nicotiana paniculata
ORGANISM Nicotiana paniculata
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (sites)
Komori, T., Yamada, S. and Imaseki, H.
A cDNA clone for gamma-thionin from Nicotiana paniculata (Accession No. AB005250) (FGR97-132)
Plant Physiol. 115, 314 (1997)
REFERENCE 2 (bases 1 to 549)
Komori, T.
Direct Submission
Submitted (26-JUN-1997) Toshiyuki Komori, Plant Breeding and Genetic Research Laboratory, Japan Tobacco Inc., 700 Higashibara, Iwate, Shizuoka 438, Japan
[E-mail: Toshiyuki.Komori@pbgrl.jti.co.jp, Tel: 0538-32-7116, Fax: 0538-32-8700]
JOURNAL Location/Qualifiers
FEATURES
source
1. 549
/organism="Nicotiana paniculata"
/mol_type="mRNA"
/db_xref="taxon:62141"
1. 549
/gene="NpThio1"
48. 368
/gene="NpThio1"
/codon_start=1
/product="gamma-thionin"
/protein_id="BA21325.1"
/db_xref="GI:2251081"
/translation="MARSLCFMAFPAVLAMMFLPAYEVOAKSTKASNTFPGICITKPK
PERKACISEKFTDGHCSKILRRCLCTKPCVDEKMIQTGAENLAEAEETLAAALLLEEI
MMDN"

BASE COUNT 166 a 87 c 112 g 184 t

ORIGIN

Query Match 18.2%; Score 92; DB 8; Length 549;
Best Local Similarity 57.1%; Pred. No. 1.7e-09;
Matches 275; Conservative 0; Mismatches 160; Indels 47; Gaps 4;

QY 1 AAAGAGCTATGCTGCTGCTTCATTACTTCATGCGATTTCTTGTCTTGGCAATGACATC 60
DB 39 AAAGAACTATGCTGCTGCTTCATTACTTCATGCGATTTCTTGTCTTGGCAATGACATC 98
QY 61 TTGTTGCTTATGGGTGCAAGGCAAGAAATTTGCTTAAAGGCTCACAAACCTGTT 120

Db	99	TTTGGTGCCTA*GAGGTGCAGAGCTAAGAGTACTTGCAAGCAGAAACATATACATTCCT	158
Qy	121	AAATGCTTACAGTACCCCTCTATGTCTAAAACCTCTGTATGAGAGAGGAATATGAAAT	180
Db	159	GGAATATGCAATTAACMAACACCATGACGAAAAAGCTGTCTCAAGTGGAAATTTACTGAT	218
Qy	181	GGTCATTGTTTCACATCCTTAAGCAAGTCTTATGATGATGAAGATG-----TAATGCT	234
Db	219	GGAATAATGACGAAATCCTCAGAAAGTGCATTTGCTACAAAGCATGTGTATTTGATGCA	278
Qy	235	AAAAGTCTGCGAACAGAAATTGC-----	256
Db	279	AAGATGATCAAAACAGAGACTGAAAAATTTGGCCGAGAGACAGAACTTTGGCTGCAGCT	338
Qy	257	TTGCTTGAAGAAGAGTTCCTCAAGAGATATTAAGTTGATATGATGATTAG--TGTCAC	314
Db	339	TTGCTTGAAGAAGAGTGTGATGATTAAGTATTAAGATATTAAGAAATTTAAGGATTAAGCT	398
Qy	315	ACAAATTAATTAAGTGTGGCTTTCTTAAAGGGTAACATTATATGTTGTAATCTTGG	374
Db	399	GTGCACACATATTAAGTGTGCTCTTTCTTAAAGTGAAGCTAAATGTTGTCTTATGGA	458
Qy	375	TGTATAGTACCACTTTGACACATTAATTAAGTTGTGACATCAATCTTCATGATATC	434
Db	459	CTTTTAGTACCGCTTTGTTACACTTTAATAAAG--TGAGGACATCAATCCTTGTACTT	517
Qy	435	TT 436	
Db	518	TT 519	

RESULT #	LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
AB005266	AB005266	Nicotiana excelsior mRNA for gamma-chitin, complete cds.	558 bp	linear	PLN 05-FEB-1999					
AB005266	AB005266	AB005266.1	GI:2244704	Gamma-chitin.	Nicotiana excelsior	Nicotiana excelsior	Ekharaya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.	1 (cites)	Yamada, S., Komori, T. and Tanesaki, H.	CNA cloning of gamma-chitin from Nicotiana excelsior (Accession No. AB005266) (PCR97-131)
									Plant Physiol.	115, 314 (1997)
									2 (bases 1 to 558)	
									Yamada, S.	
									Direct Submission	
									Submitted (26-JUN-1997)	
									Shigehiro Yamada, Plant Breeding and	
									Genetics Research Laboratory, Japan Tobacco Inc., 700 Higashibara,	
									Iwate, Shizuoka 438, Japan	
									E-mail:Shigehiro.Yamada@pdgr1.jti.co.jp, Tel:0538-32-7116,	
									Fax:0538-32-8700)	

FEATURES		SOURCE		Location/Qualifiers	
		1..558			
		/organism="Nicotiana excelsior"			
		/mol_type="rRNA"			
		/db_xref="taxon:61185"			
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		/db_xref="GI:2244705"			
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		MNN"			
BASE COUNT		170 a	94 c	108 g	186 t

ORIGIN	Query Match	18.2%	Score 92	DB 8	Length 558
	Best Local Similarity	65.8%	Pred. No. 1.7e-09		
	Matches 150	Conservative 0	Mismatches 75	Indels 3	Gaps 1
QY	1	AAAGAGCATATGGCTCGTTCGATTTACTTACATAGCATTTCTTCTTGGCAATGACATCTC	60		
Db	24	AAAGTAACTATGGCTCGCTCCGTGTGCTTCATGGCATTTGCTATCTTGGCAATGATGCTC	83		
QY	61	TTTGTGCTTATGGGGTGCAGAGCAAGAAATTGGCTGTAAAGAGTCCAAAGCTGT	120		
Db	84	TTTGTGGCTATGATGATGTGGAAGCTTAAAGATTTGCCAAACAGAAAGCATATCATTTCCCTGGA	143		
QY	121	AAATGTTCTAGTGACCCCTCTATGTCAAAACTCTGTATATGAGAGAGGAAATATGAGAT	180		
Db	144	ATATGCAATTACCAAAACCCAGCATGACAGAAAAGCTGTAT---CAAGAGAAATTTTACTGT	200		
QY	181	GGTCATTTGTTTCACATTCCTAAGCAAGTGCCTTATGATATGAAGAGATGT	228		
Db	201	GGTCATTTGAGCAAAATCTCTAGAAAGGAGTCTATATGACCTAAGGCAATGT	248		

RESULT 9	
AB005265	
LOCUS	
DEFINITION	AB005265 448 bp mRNA linear PLN_04-JUL-1997.
ACCESSION	AB005265
VERSION	AB005265.1 GI:2244702
KEYWORDS	gamma-chionin,
SOURCE	Nicotiana excelsior
ORGANISM	Nicotiana excelsior
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; lamiales; Solanales; Solanaceae; Nicotiana. 1 (sites)
AUTHORS	Yamada,S., Komori,T. and Imaseki,H.
TITLE	cDNA cloning of gamma-chionin from Nicotiana excelsior
JOURNAL	Unpublished 2 (bases 1 to 448) Yamada,S.
REFERENCE	Direct Submission
TITLE	Submitted (26-JUN-1997) Shigehito Yamada, Plant Breeding and Genetics Research Laboratory, Japan Tobacco Inc.; 700 Higashihara, Iwata, Shizuoka 438, Japan
JOURNAL	[E-mail:]Shigehito.Yamada@pbgrl.jti.co.jp, Tel:0538-32-7116, Fax:0538-32-8700]

FEATURES	
source	Location/Qualifiers
gene	1..448 /organism="Nicotiana excelsior" /mol_type="mRNA" /db_xref="taxon:61185"
CDS	1..448 /gene="Nethiol1" <1..240 /gene="Nethiol1" /codon_start=1 /product="gamma-L-cholinin" /protein_id="PAA21113.1" /db_xref="GI:2244703" /translation="LIVAEYVQARQCARLPMGLCTINPQCKKACIKKFTDHSCKSLRRCLCTPRCTGCAFTLAEENTTAAALLLEEDINDN"
BASE COUNT	141 a 73 c 88 g 146 t
ORIGIN	
Query Match	13.3%; Score 67.2; DB 8; Length 448;
Best Local Similarity	56.2%; Pred. No. 0.00031;
Matches 244; Conservative	0; Mismatches 158; Indels 32; Gaps 5;
Oy	58 CTCCTTTGTCCTATAGGGTCGAAGGCAGAGAAATTGCTGTAAAGAGCTCAAAACCT 117
db	1 CTCCTTGTTCCTATAGAGAGTCGAAGCTAAGAAATTTTCA-----CT 54

Oy	118	GTGTAAGTCTCTAGTACCCCTCTATGTCACAAAACCTGTATGAGAAAGAGAAATATGAA	177
Db	55	GGACTATGCAATTACCAATCCACATGACAAAAGCTGTAT---CMAAGAAATTTACT	111
Oy	178	GATGTCATTGTTTTCACAAATCCTTAAGCAAGTCTTATGATGAAAGAGATGTAAT--GCT	234
Db	112	GATGTCATTGTTAGCAAAATCCTCAGAAGGTGTCTATGACTTAACCCATGACAGAGACT	171
Oy	235	AAAACCTGCCAACAGAAATTC-----TTGCTTGAAGAAAGATTCCTC	277
Db	172	GAACCTTTACTGAGGAGAAAGCAACATTGGCTGCAGCTTGTCTGAAAGAAAGATATATG	231
Oy	278	AAGCAGTAATTAAGTTTGATGATGATTTAG---TGTCACAAATAATTAATAAGTGT	334
Db	232	GATACACTATAGAGATTAAGATTAATTAATTAAGATGAGACATGACACATTAATTAAGTTCT	291
Oy	335	GCCCTTCTTAAAGGGTAACCTTAATTAATGTTGATTTCTGGTGATATAGTAGCCATTGACA	394
Db	292	ACCTTCTTTAAAGGTAGCTATGTTGTTGTTTAAATGAGCTTTAGAGCCTTTAATA	351
Oy	395	CATTAAATTAAGTTGTGACACATCAATCTTCATGATCTTCTATTAAGTTGTGTGT	454
Db	352	CACTTTAATTAAGTGTGGACATTCACCCCTTGTGCAATCTTGACCTAAAGTTTATGTGTG	411
Oy	455	TTAATGAAAGAGA	468
Db	412	TACTTTAATGAAA	425

RESULT 10
PMAIL7P1_05/C

WPCOMMENT
Sequence split into 14 fragments LOCUS PFWAL7P1 Accession AL844506

Fragment Name	Begin	End
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PFMAL7P1_02	200001	310000
PFMAL7P1_03	300001	410000
PFMAL7P1_04	400001	510000
PFMAL7P1_05	500001	610000
PFMAL7P1_06	600001	710000
PFMAL7P1_07	700001	810000
PFMAL7P1_08	800001	910000
PFMAL7P1_09	900001	1010000
PFMAL7P1_10	1000001	1110000
PFMAL7P1_11	1100001	1210000
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	Matches 119;	Conservative	0;	Mismatches 105;	Indels 0;	Gaps 0;
QY	283	GTATTAATTTGATTATGATTTAGTGACACAAAATTAATTAATTAATGTTGCCTTC	342			
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QY	343	TAAATACGGTACTTAAATGTTGATCTCTGGTGTATGACCTTTGAACACTTAAAT	402			
DB	29307	TAAACCTTAAGATATATATATGTTCTTTATTTAATTTAAAAATATATATAAAT	29248			
QY	403	TAAAGTTTGACACTCAATCTCTCATGATCTCTTATTAAGTTGTGTGTTTAATGA	462			
DB	29247	TTAAATATATTCAAAATTAATCTTTTAAAAAATAAGAAAAATTTTATAGATATTTAATTA	29188			
QY	463	AAGAGATCGTTTAGCGTCTTAAAAAATAAAAAATAAAAA	506			
DB	29187	TATGCTTAATACGACACCGGAAAAAATAAAAAATAAAAA	29144			

RESULT 11
AC116988

LOCUS	AC116988	331039 bp	DNA	linear	INV 12-MAR-2003			
DEFINITION	Dictyostelium discoideum chromosome 2 map 6445720-6776760 strain AX4, complete sequence.							
ACCESSION	AC116988							
VERSION	AC116988.2	GI:28829381						
KEYWORDS	HTG.							
SOURCE	Dictyostelium discoideum							
ORGANISM	Dictyostelium discoideum							
REFERENCE	Bukacynska, M., & Flegler, A. (2003) Dictyostelium discoideum 1 (bases 1 to 331039)							
AUTHORS	Glockner, G., Eichinger, L., Szefranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., Appl, J. F., Guiso, R., Kumpf, K., Tungal, B., Cox, E., Quail, M. A., Platzer, M., Rosenthal, A. and Noegel, A. A.							
TITLE	Sequence and analysis of chromosome 2 of Dictyostelium discoideum							
JOURNAL	Nature 418 (6893), 79-85 (2002)							
MEDLINE	22092622							
PUBMED	12097910							
REMARK	The Dictyostelium Genome Sequencing Consortium							
REFERENCE	2 (bases 1 to 331039)							
AUTHORS	Baumgart, C.							
TITLE	Direct Submision							
JOURNAL	Submitted (05-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany							
REFERENCE	3 (bases 1 to 331039)							
AUTHORS	Baumgart, C.							
TITLE	Direct Submision							
JOURNAL	Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany							
REFERENCE	4 (bases 1 to 331039)							
AUTHORS	Baumgart, C.							
TITLE	Direct Submision							
JOURNAL	Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany							
COMMENT	On Mar 4, 2003 this sequence version replaced gi:20042960. CDS predictions from Geneid do not necessarily reflect true genes. Further information is available from IMB Jena, Department of Genome Analysis							
	(http://genome.imb-jena.de/dictyostelium/) and the University Cologne, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml							
	Funding Agency : Deutsche Forschungsgemeinschaft (DFG).							
FEATURES	Location/Qualifiers							
SOURCE	1..331039							

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complement(join(2345..3098,3189..3526))
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AC118276/c AC118276 51729 bp DNA linear PRI 29-MAY-2002
 LOCUS Homo sapiens BAC clone RP11-115F20 from 2, complete sequence.
 DEFINITION AC118276
 AC118276
 VERSION AC118276.3 (20429585
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 51729)
 AUTHORS Sulston, J.E., and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074
 REFERENCE 2 (bases 1 to 51729)
 AUTHORS Coyne, E. and Kozlowski, A.
 TITLE The sequence of Homo sapiens BAC clone RP11-115F20
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 51729)
 AUTHORS Waterston, R.H.
 TITLE Direct Submision
 JOURNAL Submitted (14-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 51729)
 AUTHORS Waterston, R.H.
 TITLE Direct Submision
 JOURNAL Submitted (20-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 5 (bases 1 to 51729)
 AUTHORS Waterston, R.H.
 TITLE Direct Submision
 JOURNAL Submitted (03-MAY-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 6 (bases 1 to 51729)
 AUTHORS Waterston, R.
 TITLE Direct Submision
 JOURNAL Submitted (29-MAY-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT On May 3, 2002 this sequence version replaced gi:2017775.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: saplens@wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0115F20

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>
 SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateo, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-34405, 2000 bp overlap; the clone sequenced to the right is RP11-49215, 2000 bp overlap.
 Actual end of this clone is at base position 68541 of RP11-49215.

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	/map="2"
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	/clone_11b="RP11-11"
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repeat_region	1145. 1267
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repeat_region	2454. 2542
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repeat_region	2990. 3051
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DB 20510 ATGAGCTTAATTAAGTGTTCCTTTTAAAGGTAAGTAAATGTTGATTC 20451
QY 375 TGTATAGTACCACTTGCACATTAATTAAGTGTGACACATTCCTTGATTC 434
DB 20450 AGAGAGAGTAACAGTGAAGCACTCAATGACATTTTAAATTAATTAAT 20391
QY 435 TTTATTAAGTGTTCGTTTAAATGAAGATCGTTTACGGTCTAAATTAATTA 494
DB 20390 ATTAATGCTATGTAAGAGTACATGAAGTCTATTGACATACGTAAAAA 20331
QY 495 AAAAAAAAAA 506

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Db 20330 AAAAAAAAAA 20319
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RESULT 13
PFA929358 254050 bp DNA linear INV 29-JAN-2003
LOCUS PFA929358
DEFINITION Plasmodium falciparum strain 3D7, chromosome 9, segment 4/5.
ACCESSION AL929358 AL844508
VERSION AL929358.1 GI:23505147
KEYWORDS
SOURCE Plasmodium falciparum 3D7
ORGANISM Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
REFERENCE 1 (bases 1 to 254050)
AUTHORS Hall, N., Pain, A., Bertman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Buckee, C.O., Burrows, C., Cherevach, I., Chillingworth, C., Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Corcoran, C., Cronin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Felwell, T., Goble, A., Goodhead, I., Gwilliam, R., Hamlin, R., Hance, Z., Harper, D., Hauser, H., Hornsbury, T., Holroyd, S., Horrocks, P., Humphrey, S., Jagels, K., James, K.D., Johnson, D., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Leonard, N., Line, A., Maddison, M., McLean, J., Mooney, P., Moulé, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Rabinowitsch, E., Rajandream, M.A., Rutter, S., Rutherford, K.M., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Squares, S., Stevens, K., Taylor, K., Tiley, A., Unwin, L., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrett, B.G.
TITLE Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
JOURNAL Nature 419 (6906), 527-531 (2002)
MEDLINE 22255708
PUBMED 12368867
AUTHORS Sanders, M., Hauser, H., Baker, S., Unwin, L., Mungall, K., Bertman, M., Pain, A., Hall, N., Bowman, S., Churcher, C., Quail, M. and Barrett, B.
TITLE Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium, The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
COMMENT For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/projects/P_falciparum.
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probability 0.995) with cleavage site probability 0.001
between residues 27 and 28
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origin; N-terminal signal peptide. Similar to Lactococcus
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35.21% id in 213 aa, and to Escherichia coli prollyl-tRNA
synthetase pros or dips or b0194 SMALL:SYF_ECOLI
(SMALL:P16659) (572 aa) fasta scores: E(): 7.3e-08, 31.91%
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II (G, H, P, S and T)
Signal peptide predicted for PF11240c by SignalP 2.0 HMM
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probability 0.018) with cleavage site probability 0.591
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Matches 154; Conservative 0; Mismatches 149; Indels 2; Gaps 1;

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Db 7976 TTTATATAAATTTATATCTTACACAAATGAATTTTATTTTATTTTCAATCACA 8035
Oy 398 TAAATTAAGTTGTGACATCAATCTTCATGATCTTCAATTAAGTTGTGTTTAA 457
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Oy 458 ATGAA 462
Db 8096 ATGTA 8100

RESULT 14
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WPCOMMENT
Sequence split into 6 fragments LOCUS AC116984 Accession AC116984
Fragment Name Begin End
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AC116984_1 100001 210000
AC116984_2 200001 310000
AC116984_3 300001 410000
AC116984_4 400001 510000
AC116984_5 500001 541399
Continuation (4 of 6) of AC116984 from base 300001 (AC116984 Dictyostelium discoideum ch

Query Match 10.3%; Score 52.2; DB 3;
Best Local Similarity 52.5%; Pred. No. 0.17; Length 110000;
Matches 114; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Oy 285 AATTAGTTGATTAAGTATAGTGCACACAAATTAATTAAGTGTGCTTCTTA 344
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Db 14280 AGTGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 14221
Oy 405 AAGTTGACATCATCTCATGATCTTCAATTAAGTTGTGTTTAAATGAAA 464
Db 14220 TACATTAATCATCTCATGATTTTGAATTTTCTTTTCTTTTCTTTTAAATCAA 14161
Oy 465 GAGATCGTTAGCGGTAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 501
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LOCUS PFMAL3P5
DEFINITION Plasmodium falciparum MAL3P5, complete sequence.
ACCESSION AL003456 AL008971 AL008972 AL008978 AL010141 AL010153 AL010152
VERSION AL010206 AL010210 AL139179 AL844502
KEYWORDS AL034556.4 GI:23477013
SOURCE HNG; centromere; CTRP protein; initiation factor B4;
Plasmodium falciparum 3D7
ORGANISM Plasmodium falciparum 3D7
Eukaryota; Alveolates; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 86826)
AUTHORS Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T.,
Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Feltwell,T.,
Gentles,S., Gwilliam,R., Hamlin,N., Harris,B., Hooton,D.,
Hornby,T., Horrocks,P., Jagels,K., Jaseil,B., Kyes,S., McLean,J.,
Moule,S., Mungell,K., Murphy,L., Oliver,K., Rutter,S., Sutherland,K.M.,
Rajandream,M.-A., Rutter,S., Skellon,J., Squares,R., Squares,S.,
Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and
Barrell,B.G.
The complete nucleotide sequence of chromosome 3 of Plasmodium

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JOURNAL falciparum
MEDLINE Nature 400 (6744), 532-538 (1999)
PUBMED 99376085
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2
HALL,N., Pain,A., Berriam,M., Churcher,C., Harris,B., Harris,D.,
Mungell,K., Bowman,S., Atkin,R., Baker,S., Barron,A., Brooke,K.,
Buckee,C.O., Burrows,C., Cherevach,I., Chillingworth,C.,
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Sanders,M., Simmonds,M., Seeger,K., Sharp,S., Smith,R., Squares,R.,
Squares,S., Stevens,K., Taylor,K., Tivey,A., Unwin,L.,
Whitehead,S., Woodward,J., Sulston,J.E., Craig,A., Newbold,C. and
Barrell,B.G.
Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
Nature 419 (6906), 527-531 (2002)
22255708
12368867
3 (bases 1 to 86826)
Lawson,D., Bowman,S. and Barrell,B.
Direct Subsequen
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA, UK
On Oct 2, 2002 this sequence version replaced gi:7711064.
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P_falciparum.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 23, 2003, 07:07:53 ; Search time 162 Seconds
(without alignments)
1151.837 Million cell updates/sec

Title: US-09-854-562-2

Perfect score: 445
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1517243 seqs, 1124081882 residues

Total number of hits satisfying chosen parameters: 3034486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXLEN=2000000000 -USPR=US09854562.@CGN.1.1.164@runat.22082003.103831.4863
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	132	29.7	3528	9	US-09-777-347-2	Sequence 2, Appli
3	97	21.8	416	14	US-10-178-213-94	Sequence 94, Appl
4	91.5	20.6	307	14	US-10-178-213-295	Sequence 295, Appl
5	89	20.0	523	14	US-10-178-213-412	Sequence 412, Appl
6	87	19.6	363	14	US-10-178-213-124	Sequence 124, Appl
7	87	19.6	367	14	US-10-178-213-121	Sequence 121, Appl
8	86.5	19.4	272	10	US-09-878-574-10791	Sequence 10791, A
9	86.5	19.4	277	10	US-09-878-574-11794	Sequence 11794, A
10	86.5	19.4	361	10	US-09-878-574-1139	Sequence 1139, Appl
11	86.5	19.4	469	14	US-10-178-213-91	Sequence 91, Appl
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13	85	19.1	520	14	US-10-178-213-373	Sequence 373, Appl
14	83.5	18.8	275	10	US-09-878-574-14296	Sequence 14296, A
15	82	18.4	380	14	US-10-178-213-142	Sequence 142, Appl
16	81.5	18.3	447	14	US-10-178-213-136	Sequence 136, Appl
17	81	18.2	234	10	US-09-938-842A-618	Sequence 618, Appl
18	81	18.2	372	14	US-10-178-213-178	Sequence 178, Appl
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21	80	18.0	493	14	US-10-178-213-364	Sequence 364, Appl
22	79.5	17.9	538	14	US-10-178-213-382	Sequence 382, Appl
23	79	17.8	346	14	US-10-178-213-208	Sequence 208, Appl
24	79	17.8	375	14	US-10-178-213-169	Sequence 169, Appl
25	79	17.8	378	14	US-10-178-213-190	Sequence 190, Appl
26	79	17.8	398	14	US-10-178-213-160	Sequence 160, Appl
27	79	17.8	410	14	US-10-178-213-148	Sequence 148, Appl
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29	78.5	17.6	409	14	US-10-178-213-193	Sequence 193, Appl
30	78.5	17.6	517	14	US-10-178-213-467	Sequence 467, Appl
31	78.5	17.6	470	14	US-10-178-213-88	Sequence 88, Appl
32	78	17.5	385	14	US-10-178-213-151	Sequence 151, Appl
33	77.5	17.4	343	14	US-10-178-213-217	Sequence 217, Appl
34	77.5	17.4	379	14	US-10-178-213-199	Sequence 199, Appl
35	77.5	17.4	398	14	US-10-178-213-157	Sequence 157, Appl
36	77.5	17.4	416	14	US-10-178-213-115	Sequence 115, Appl
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38	77.5	17.4	432	14	US-10-178-213-211	Sequence 211, Appl
39	77.5	17.4	462	14	US-10-178-213-304	Sequence 304, Appl
40	77.5	17.4	512	14	US-10-178-213-220	Sequence 220, Appl
41	77	17.3	294	9	US-09-294-093B-3064	Sequence 3064, Ap
42	77	17.3	387	14	US-10-178-213-139	Sequence 139, Appl
43	77	17.3	410	14	US-10-178-213-136	Sequence 136, Appl
44	76.5	17.2	330	14	US-10-178-213-166	Sequence 166, Appl
45	76.5	17.2	388	14	US-10-178-213-184	Sequence 184, Appl

ALIGNMENTS

RESULT 1
US-09-777-347-1
Sequence 1, Application US/09777347
Patent No. US20010014977A1
GENERAL INFORMATION:

APPLICANT: McBride, Kevin E.

Stalker, David M.

TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Calgene, Inc.

STREET: 1920 Fifth Street

CITY: Davis

STATE: CA

COUNTRY: USA

ZIP: 95616

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.1

SOFTWARE: Microsoft Word 5.1 (a)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/777.347

FILING DATE: 05-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,087

FILING DATE: <Unknown>

APPLICATION NUMBER: USSN 07/554,195

FILING DATE: 17-JUL-90

APPLICATION NUMBER: USSN 07/382,518

FILING DATE: 19-JUL-89

ATTORNEY/AGENT INFORMATION:

NAME: Carl J. Schwedler

REGISTRATION NUMBER: 36,924

REFERENCE/DOCKET NUMBER: CGNE 91-1

TELEPHONE: (916) 753-6313

TELEFAX: (916) 753-1510

INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:

LENGTH: 564 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1

US-09-777-347-1

Alignment Scores:

Pred. No.: 9,15e-17

Score: 182.50

Percent Similarity: 62.35%

Best Local Similarity: 48.24%

Query Match: 41.01%

DB: 9

Gaps: 3

US-09-854-562-2 (1-83) x US-09-777-347-1 (1-564)

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QY 20 TyrGlyValGlnGlyLysGlnLeuLeuCys---CysLysGlnLeuThrLysProValLysCys 38

DB 100 TATGAGGTGAGAGCTCAGCAATTTGCAACACCAACCACTTCCAGCATTAATCT 159

QY 39 SerSerAspProLeuGlnLysLeuGlnLysGlnLysGlnLysGlnLysGlnLysGlnLys 58

DB 160 TTTATGACTCATCTATGAGAAATTTGTATC---AAAGAGAAATTTACTGTGAGACAT 216

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DB 217 TGTAGCAAACTCCAAAGAGTGTATGACCTAAGCATGTGTATTGACAAATCTCA 276

QY 79 ThrGlnLeuLeuAla 83

DB 277 AGTGAAGTTAAAGCA 291

RESULT 2

US-09-777-347-2

Sequence 2, Application US/0977347

Patent No. US20010014977A1

GENERAL INFORMATION:

APPLICANT: McBridge, Kevin E.

TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: Calgene, Inc.

CITY: Davis

STATE: CA

COUNTRY: USA

ZIP: 95616

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.1

SOFTWARE: Microsoft Word 5.1 (a)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/777,347

FILING DATE: 05-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,087

FILING DATE: <Unknown>

APPLICATION NUMBER: USSN 07/554,195

FILING DATE: 17-JUL-90

APPLICATION NUMBER: USSN 07/382,518

FILING DATE: 19-JUL-89

ATTORNEY/AGENT INFORMATION:

NAME: Carl J. Schwedler

REGISTRATION NUMBER: 36,924

REFERENCE/DOCKET NUMBER: CGNE 91-1

TELEPHONE: (916) 753-6313

TELEFAX: (916) 753-1510

INFORMATION FOR SEQ ID NO: 2

SEQUENCE CHARACTERISTICS:

LENGTH: 3528 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 2

US-09-777-347-2

Alignment Scores:

Pred. No.: 2.22e-08

Score: 132.00

Percent Similarity: 33.33%

Best Local Similarity: 26.42%

Query Match: 29.66%

DB: 9

Gaps: 4

US-09-854-562-2 (1-83) x US-09-777-347-2 (1-3528)

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QY 20 TyrGlyValGlnGlyLysGlnLeuLeuCys---CysLysGlnLeuThrLysProValLysCys 24

DB 2698 TATGAGGTGAGAGCTCAGCAATTTGCAACACCAACCACTTCCAGCATTAATCT 2757

QY 25 LysGlnLeuLeuCysValGlnLeuThrLys---ProValLys--- 37

DB 2758 AAGCAGACATCAGTAAACCGTTAAATTAACCTTAATAATTGATGATTAATCTT 2817

QY 37 37

DB 2818 GCTATACGTTTAACAATATGATAAAAAACCTTAATAATTAATTAATTTTCGATTCGTC 2877

QY 37 37

DB 2878 CTCCTATGTTATTTCTAATTTTGTGTGAATGATTTAGAGTGAAGCTCAGCA 2937

QY 38 38

DB 2938 AATTGCAAGACCAACCAACCACTTCCAGAGATTAATTTTATGATCATCATGAG 2997

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QY 65 sCysLeuGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLys 83

DB 3055 GTCTCTATGACCTAAGCATGTGTATTGACAAATCTCAAGTGAAGTTAAAGCA 3109

RESULT 3


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US-10-178-213-94
; Sequence 94, Application US/10178213
; Publication No. US20030041346A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cañon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensein Polynucleotides and Methods of
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
PRIOR FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 94
LENGTH: 416
TYPE: DNA
ORGANISM: Tulipa gesneriana
FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(233)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (84)...(230)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 355..380, 385, 396, 405
OTHER INFORMATION: n = A,T,C or G
US-10-178-213-94

Alignment Scores:
Pred. No.: 0.000117 Length: 416
Score: 97.00 Matches: 25
Percent Similarity: 45.45% Conservative: 15
Best Local Similarity: 28.41% Mismatches: 16
Query Match: 21.80% Indels: 12
DB: 14 Gaps: 3
US-09-854-562-2 (1-63) x US-10-178-213-94 (1-416)
QY 4 SerTLeYrPhemetaAlaPheLeuValIleuAlaThrPheValAlaIleYrGlyValGln 23
Db 27 TCTTCTCTCTTCGGTCTCTCTTACGCTGGCTTC-----GGGCTGGAGTGGAA 77
QY 24 GlyLysGluIleCysCysLysGluLeuThrLysProValLys-----CysSerSerAsp 41
Db 78 GCTAGCTCTCTGCGCGAAGGTTTGAGCAATGGGTTCAAGACTGCTTCAGCAGC 137
QY 42 ProLeuCysGlnLysLeuCysMetGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 61
Db 138 GACAAAGTGTCCAAAGTTTGCAAGACGAGCGAACCAGAGTGGTGTCTTCGGATGCG 197
QY 62 IleLeuSerLysCysLeuCysMetLysArgCys-----AsnAla 74
Db 198 GTTGGCCGTGGTGGTCAAGTGAACCAACTGCTGAACCAAGGCTTCGAGAAAGGCT 257
QY 75 LyeThrIleuAlaThrGluLeuLeu 82
Db 258 GTATCTGACTGTGTAAGTTACTC 281

RESULT 4
US-10-178-213-295
; Sequence 295, Application US/10178213
; Publication No. US20030041346A1

```

```

: GENERAL INFORMATION:
: APPLICANT: Simmons, Carl R.
: APPLICANT: Navarro Acevedo, Pedro A.
: APPLICANT: Harvell, Leslie
: APPLICANT: Cacho, Rebecca
: APPLICANT: McCutchen, Billy Fred
: APPLICANT: Lu, Albert
: APPLICANT: Hermann, Rafael
: APPLICANT: Mong, James
: TITLE OF INVENTION: Defensin Polynucleotides and Methods of
: TITLE OR INVENTION: Use
: FILER REFERENCE: 35718/246703
: CURRENT APPLICATION NUMBER: US/10/178, 213
: PRIOR FILING DATE: 2002-06-21
: PRIOR APPLICATION NUMBER: 60/300,152
: PRIOR FILING DATE: 2001-06-22
: PRIOR APPLICATION NUMBER: 60/300,241
: NUMBER OF SEQ ID NOS: 459
: SOFTWARE: PatSeq for Windows Version 4.0
: SEQ ID NO 295
: LENGTH: 307
: TYPE: DNA
: ORGANISM: Hedera helix
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (3)...(158)
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: (3)...(140)
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 263, 270, 285, 294, 301, 306
: OTHER INFORMATION: n = A,T,C or G
US-10-178-213-295

Alignment Scores:
Pred. No: 0.000469 Length: 307
Score: 91.50 Matches: 17
Percent Similarity: 57.69% Conservative: 5
Best Local Similarity: 44.74% Mismatches: 15
Query Match: 20.56% Indels: 1
DB: 14 Gaps: 1

US-09-854-562-2 (1-83) x US-10-178-213-295 (1-307)
Cy CySerSerAaPProLeuCySgInuSLeuCySmecGInuSgInuSTyrgInaPpGly 57
Db 39 TGCACGGATGATCCAGCGTGAAGAACTTTCG--GAGAAAGATGATCTTTGATGCT 95
Cy 58 HAcGcPAtHrHrIleuSerIysCySLeuCySMeTlySaGcCySaMaLaLys 75
Db 96 CACTGCGTCGCGCTTATTACAAAATGTTATTGCGCGCTGGAATTGTCCGCAAAA 149

RESULT 5
US-10-178-213-412
: Sequence 412, Application US/10178213
: Publication No. US20030041348A1
: GENERAL INFORMATION:
: APPLICANT: Simmons, Carl R.
: APPLICANT: Navarro Acevedo, Pedro A.
: APPLICANT: Harvell, Leslie
: APPLICANT: Cacho, Rebecca
: APPLICANT: McCutchen, Billy Fred
: APPLICANT: Lu, Albert
: APPLICANT: Hermann, Rafael
: APPLICANT: Mong, James
: TITLE OF INVENTION: Defensin Polynucleotides and Methods of
: TITLE OR INVENTION: Use
: FILER REFERENCE: 35718/246703
: CURRENT APPLICATION NUMBER: US/10/178, 213
: PRIOR FILING DATE: 2002-06-21
: PRIOR APPLICATION NUMBER: 60/300,152
: PRIOR FILING DATE: 2001-06-22
: PRIOR APPLICATION NUMBER: 60/300,241
: NUMBER OF SEQ ID NOS: 459
: SOFTWARE: PatSeq for Windows Version 4.0
: SEQ ID NO 295
: LENGTH: 307
: TYPE: DNA
: ORGANISM: Hedera helix
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (3)...(158)
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: (3)...(140)
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 263, 270, 285, 294, 301, 306
: OTHER INFORMATION: n = A,T,C or G
US-10-178-213-295

```

```

APPLICANT: Stmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harrell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensin Polynucleotides and Methods of
FILE OF INVENTION: Use
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows, Version 4.0
SEQ ID NO 121
LENGTH: 367
TYPE: DNA
ORGANISM: Momordica charantia
FEATURE:
NAME/KEY: CDS
LOCATION: (71)...(265)
FEATURE:

```

```

US-10-178-213-91
Alignment Scores:
Pred. No.: 0 00447
Score: 86.50
Percent Similarity: 45.07%
Best Local Similarity: 29.58%
Query Match: 19.44%
DB: 14
Gaps: 2
US-09-854-562-2 (1-83) x US-10-178-213-91 (1-469)
Qy 4 SerIleTyRPhenMetAlaPheLeuValIeuAlaThrIeuPheValAlaIaTyRcIyValcIn 23
Db 27 TCTTTCCTTCCTCGCGTTCCTCTTACTGCTGCGCTTCT-----GGCGCTGAATTGAA 77
Qy 24 GlyLysGluIleCysCysLysGlnIuLeuThrIyRProValIys-----CysSerSerAsp 41
Db 78 GCGTGTCTCTCTCGCGAAGGAGGTTTCGAGCAATGGTTCAAAAGACTGTGCTTCAGCAGC 137
Qy 42 ProLeuCySgLnIySeuCySmetGtIuSgIuIyRcIuAspIyHIsCyPheThr 61
Db 138 GACAAGTGTGCAAGGAGTTTGATGAGCCAGCAACCGCAGGGCGGTTTCTTGCGATGCC 197
Qy 62 IleLeuSerIyScySLeuCySmetIyRAsyRys 72
Db 198 ATTGCGCGTCTGCGATGTGTAAGCCAAACTGC 230
RESULT 12
US-10-178-213-385
Sequence 385, Application US/10178213
Publication No. US20030041348A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensin Polynucleotides and Methods of
TITLE OF INVENTION: Use
FILE REFERENCE: 35716/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 385
LENGTH: 466
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: CDS
LOCATION: (33) ... (267)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (126) ... (266)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 430
OTHER INFORMATION: n = A,T,C or G
US-10-178-213-385
Alignment Scores:
Pred. No.: 0 00727
Score: 85.00
Percent Similarity: 42.50%
Best Local Similarity: 28.75%
Length: 466
Matches: 23
Conservative: 11
Mismatch: 34
Indels: 5
Gaps: 2

```

Query Match: 19.10% Indels: 8
DB: 14 Gaps: 3

US-09-854-562-2 (1-83) x US-10-178-213-385 (1-466)

Qy 1 MetAlaSerSerle-----TyrPheMetAlaPheLeuValLeuAlaThr 15
DB 33 ATGGCTCGCTCAAGTGGCTTGTTCACACATTTTGTCTTCTTCTTCTGATAGCC 92
Qy 16 LeuPheValAlaTyrGlyValGlnGlyGluLeuLeuTyrGlySerPro 35
DB 93 ACCGAGATGGGGCCACATGCTGGCAGACAGAACATCTGTGATCTCAGACCATCTGT 152
Qy 36 ValIys-----CysSerSerAspProLeuCysGlnLysLeuCysMetGluLysGluLys 53
DB 153 TTCAAGGGGCGCATGTTTAAGTACACACACATGCTGCTCTTCTTCC---CGAACCGAAGGT 209
Qy 54 TyrGluAspGlyHisCysPheThrIleLeuSerLysCysLeuCysMetLysArgCysAsn 73
DB 210 TTCTCTGGAGGACACTGCGCTTTCAGTGCAGATGCTTCTGACCAAGATGTAAAT 269

RESULT 13
US-10-178-213-373
Sequence 373, Application US/10178213
Publication No. US20030041348A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McClutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Hermann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensein Polynucleotides and Methods of
TITLE OF INVENTION: Use
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FaetsEQ for Windows Version 4.0
SEQ ID NO 373
LENGTH: 520
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: CDS
LOCATION: (3) ... (467)
FEATURE:
NAME/KEY: mat peptide
LOCATION: (213) ... (359)
US-10-178-213-373

Alignment Scores:
Pred. No.: 0.00849 Length: 520
Score: 85.00 Matches: 19
Percent Similarity: 46.43% Conservative: 7
Best Local Similarity: 33.93% Mismatches: 20
Query Match: 19.10% Indels: 10
Gaps: 3

US-09-854-562-2 (1-83) x US-10-178-213-373 (1-520)

Qy 26 GluIleCysCysLysGlu-----LeuThrLysProValIys 37
DB 195 GAGAAATTGGCTGAGTGCAGCTTGTCTTAACCAAAATGGCCCTTGATATCGCGGAGAG 254
Qy 38 CysSerSerAspProLeuCysGlnLysLeuCysMetGluLysGluLysTyrGluAspGly 57

DB 255 TGCAGGGGCGCAACAGAACTGGCCCATGATCTGCTCCAC---GAGAGATACACCGGCGGC 311
Qy 58 HisCysPheThr---IleLeuSerLysCysLeuCysMetLysArgCys 72
DB 312 TACTGCTCCAGGCGCTCTCTCCAGTGCATGACCAAGCGGATGT 359

RESULT 14
US-09-878-574-14296
Sequence 14296, Application US/09878574
Patent No. US2002010548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 14296
LENGTH: 275
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701068578H1
US-09-878-574-14296

Alignment Scores:
Pred. No.: 0.00567 Length: 275
Score: 83.50 Matches: 18
Percent Similarity: 46.48% Conservative: 15
Best Local Similarity: 25.35% Mismatches: 35
Query Match: 18.76% Indels: 3
Gaps: 2

US-09-854-562-2 (1-83) x US-09-878-574-14296 (1-275)

Qy 4 SerIleTyrPheMetAlaPheLeuValLeuAlaThrLeuPheValAlaTyrGlyValGln 23
DB 1 ACCATTTTCTCTCTGCTTCTGCTTCTGCTGACCTGATGATGGGCGCAACATGGTG 60
Qy 24 GlyLeuGluIleCysCysLysGluLeuThrLysProValIys-----CysSerSerAsp 41
DB 61 GCAGAGCAAGAAACTGAGTGCAGACGACCAACCGTTTCAAGGGGCGCATTTGAGTGCAC 120
Qy 42 ProLeuCysGlnLysLeuCysMetGluLysGluLysTyrGluAspGlyHisCysPheThr 61
DB 121 ACCAATGAGCTCTGTTTGC---CGAACCAACGTTTCTGAGAGACATGCGCTGCGC 177
Qy 62 IleLeuSerLysCysLeuCysMetLysArgCys 72
DB 178 TTCTGTGCGAGATGCTTCTGACCAACATTTGT 210

RESULT 15
US-10-178-213-142
Sequence 142, Application US/10178213
Publication No. US20030041348A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McClutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Hermann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensein Polynucleotides and Methods of
TITLE OF INVENTION: Use
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
CURRENT FILING DATE: 2002-06-21

GenCore version 5.1.6
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OM protein - nucleic acid search, using frame_plus_p2n model

Run on: August 23, 2003, 07:03:33 ; Search time 1918 Seconds
(without alignments)
1051.758 Million cell updates/sec

Title: US-09-854-562-2
Perfect score: 445
Sequence: 1 MASIFMAFLVATLTVAV.....SKCLCMKRCNAKTLATLELLA 83

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-O=/cgm2_1/USFTO.spool/US09854562/runat.22082003.1038304817/app_query.fasta.1.263
-DB=EST -QMT=fastap -SUFIT=22n.rst -MINMATCH=0 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptc -NORM=exc -HMAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09854562 @CGM 1.1 2135 @runat.22082003.1038304817 -NCPU=6 -ICPU=3
-NO MAP -LARGEJOINT -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAP TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST :
1: em_estba :
2: em_esthum :
3: em_estin :
4: em_estnu :
5: em_estov :
6: em_estpl :
7: em_estro :
8: em_hic :
9: gb_est1 :
10: gb_est2 :
11: gb_hic :
12: gb_est3 :
13: gb_est4 :
14: gb_est5 :
15: em_estfun :
16: em_estom :
17: em_ges_hum :
18: em_ges_inv :
19: em_ges_pln :
20: em_ges_vrt :
21: em_ges_fun :
22: em_ges_mam :
23: em_ges_mus :
24: em_ges_pro :
25: em_ges_rtd :
26: em_ges_phg :
27: em_ges_vr1 :
28: gb_gsa1 :

29: gb_gsa2 :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	434.5	97.6	448	12	BM063616
2	434.5	97.6	506	14	CB164889
3	427.5	96.1	416	14	CB164909
4	427.5	96.1	633	14	CB164987
5	425.5	95.6	332	14	CB164858
6	425.5	95.6	527	12	BM064680
7	425.5	95.6	648	14	CB185066
8	425	95.5	530	12	BM062133
9	422.5	94.9	496	14	CB164824
10	421.5	94.7	720	14	CB185076
11	329.5	74.0	231	9	AF082706
12	329.5	74.0	521	14	CA524161
13	329.5	74.0	535	12	BM062737
14	329.5	74.0	540	12	BM063527
15	329.5	74.0	545	14	CA525505
16	329.5	74.0	580	12	BM065064
17	318.5	71.6	474	14	CA525605
18	309	69.4	339	12	BM060748
19	309	69.4	447	14	CA524497
20	309	69.4	466	12	BM063884
21	309	69.4	474	14	CA514352
22	309	69.4	481	12	BM064296
23	309	69.4	509	12	BM061371
24	309	69.4	522	12	BM064663
25	309	69.4	532	12	BM063609
26	309	69.4	537	12	BM064540
27	309	69.4	571	14	CA515866
28	308	69.2	306	14	CA517625
29	304	68.3	337	14	CA514064
30	302	67.9	380	14	CA514462
31	298	67.0	376	12	BM062401
32	262	58.9	318	14	CA516127
33	237.5	53.4	500	12	BM061668
34	223	50.1	536	12	BM063253
35	217.5	48.9	513	12	BM063138
36	217.5	48.9	574	12	BM067544
37	217.5	48.9	572	12	BM064987
38	203.5	45.7	573	14	CA523446
39	185.5	41.7	419	9	AM399651
40	185.5	41.7	421	9	A1898075
41	183.5	41.2	207	12	BM059656
42	182.5	41.0	333	9	AM623112
43	182.5	41.0	378	9	A1487824
44	182.5	41.0	477	9	A1897392
45	182.5	41.0	480	9	A1490243

ALIGNMENTS

RESULT 1
BM063616
LOCUS KS01057808 KS01 Capsicum annuum 448 bp mRNA linear EST 11-SEP-2002
DEFINITION BM063616
ACCESSION BM063616
VERSION BM063616.1 GI:22783734
KEYWORDS
SOURCE Capsicum annuum
ORGANISM Capsicum annuum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 448)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
1 (bases 1 to 416)
Lee, S.J., Lee, M.Y., Lee, P.S., Choi, S.H. and Harn, C.H.
EST fragments generated by SSH of SIRO red- SBV red

Unpublished
Contact: Chee Hark Harn
Biotechnology center
NONG WOONG BIO CO., LTD.
537-17 Jeongdan, Ganam, Yeosu, Kyonggi 469-885, Republic of Korea
Tel: 82 31 883 7055
Fax: 82 31 884 7065
Email: chharn@nongwoobio.co.kr
Seq primer: T7.

FEATURES

Location/Qualifiers
1..416
/organism="Capsicum annuum"
/mol_type="mRNA"
/cultivar="SIRO, SBV"
/db_xref="taxon:4072"
/sex="thermaphrodite"
/tissue_type="fruit"
/dev_stage="mature red"
/note="Vector: pGEM-T easy, Site 1: EcoRI, SIRO red - SBV red suppression subtractive cDNA library of Hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."

BASE COUNT 126 a 70 c 95 g 135 t
ORIGIN

Alignment Scores:

Pred. No.: 2,72e-44 Length: 416
Score: 427.50 Matches: 82
Percent Similarity: 97.62% Conservative: 0
Best Local Similarity: 97.62% Mismatches: 1
Query Match: 96.07% Indels: 1
DB: 14 Gaps: 1

US-09-854-562-2 (1-83) x CB164987 (1-416)

QY 1 MchlaargserllyrPhemelaPhleuvalleuala---ThrluPhelvala 19
Db 78 ATGGCTGGTTCATTACTTCATGCGATTCATGCTTGCAATGACCCCTCTTGCT 137
QY 20 TycglvalglnlylsglnlylscysylsglnleuThrlvsprovallyscys 39
Db 138 TATGGGGGCAAGGCAAGAAATTCCTGTAAGAGCTCAAAAACCTGTTAAATGTTCT 197
QY 40 SeraspProleucysglnlylscysMetglnlylsglnlylsglnlylsglnlyl 59
Db 198 AGTACCCCTATGTCAAAACCTGTAAGAGAGAAATATGAAGATGTCATTGT 257
QY 60 PheThrlleuSerlyscysleucysMetlysaGysaanaalyethrlleualaTh 79
Db 258 TTCAATCTTAAGCAAGTCTTATGATGAAGAGATGTAATGCTTAACCTCGCAACA 317
QY 80 GluleuLeuala 83
Db 318 GAATGCTGCT 329
RESULT 4
LOCUS CB164987 633 bp mRNA linear EST 30-JAN-2003

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

K06005832 KS06 Capsicum annuum cDNA, mRNA sequence.
CB164987
CB164987.1 GI:28151113
EST.
Capsicum annuum
Capsicum annuum

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
1 (bases 1 to 633)
Lee, S.J., Lee, M.Y., Lee, P.S., Choi, S.H. and Harn, C.H.
EST fragments generated by SSH of SIRO red- SIRO green/red

Unpublished
Contact: Chee Hark Harn
Biotechnology center
NONG WOONG BIO CO., LTD.
537-17 Jeongdan, Ganam, Yeosu, Kyonggi 469-885, Republic of Korea
Tel: 82 31 883 7055
Fax: 82 31 884 7065
Email: chharn@nongwoobio.co.kr
Seq primer: T7.

FEATURES

Location/Qualifiers
1..633
/organism="Capsicum annuum"
/mol_type="mRNA"
/cultivar="SIRO"
/db_xref="taxon:4072"
/sex="thermaphrodite"
/tissue_type="fruit"
/dev_stage="mature red, green/red"
/note="Vector: pGEM-T easy, Site 1: EcoRI, SIRO red - SIRO green/red suppression subtractive cDNA library of Hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."

BASE COUNT 212 a 103 c 118 g 197 t
ORIGIN

Alignment Scores:
Pred. No.: 4,76e-44 Length: 633
Score: 427.50 Matches: 82
Percent Similarity: 97.62% Conservative: 0
Best Local Similarity: 97.62% Mismatches: 1
Query Match: 96.07% Indels: 1
DB: 14 Gaps: 1

US-09-854-562-2 (1-83) x CB164987 (1-633)

QY 1 MchlaargserllyrPhemelaPhleuvalleuala---ThrluPhelvala 19
Db 83 ATGGCTGGTTCATTACTTCATGCGATTCATGCTTGCAATGACCCCTCTTGCT 142
QY 20 TycglvalglnlylsglnlylscysylsglnleuThrlvsprovallyscys 39
Db 143 TATGGGGGCAAGGCAAGAAATTCCTGTAAGAGCTCAAAAACCTGTTAAATGTTCT 202
QY 40 SeraspProleucysglnlylscysMetglnlylsglnlylsglnlylsglnlyl 59
Db 203 AGTACCCCTATGTCAAAACCTGTAAGAGAGAAATATGAAGATGTCATTGT 262
QY 60 PheThrlleuSerlyscysleucysMetlysaGysaanaalyethrlleualaTh 79
Db 263 TTCAATCTTAAGCAAGTCTTATGATGAAGAGATGTAATGCTTAACCTCGCAACA 322
QY 80 GluleuLeuala 83

Db 323 GAATTGCTCT 334

RESULT 5
CB164858 332 bp mRNA linear EST 30-JAN-2003
DEFINITION KS05009070 KS05 Capsicum annuum cDNA, mRNA sequence.
ACCESSION CB164858
VERSION CB164858.1 GI:28150984
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 332)
Lee, S.-J., Lee, M.-Y., Lee, P.-S., Choi, S.-H. and Hahn, C.-H.
EST fragments generated by SSH of SIRO red - SBV red
JOURNAL Unpublished
COMMENT Contact: Chee Hark Harn
Biotechnology Center
NONG WOOL BIO CO., LTD.
537-17 Jeongdan, Ganam, Yeosu, Jeonnam, 546-885, Republic of Korea
Tel: 82 31 883 7055
Fax: 82 31 884 7065
Email: chharn@nongwoobio.co.kr
Seq primer: T7.

FEATURES
Location/Qualifiers
1..332
/organism="Capsicum annuum"
/mol_type="mRNA"
/cultivar="SIRO, SBV"
/db_xref="taxon:4072"
/sex="hermaphrodite"
/tissue_type="Fruit"
/dev_stage="mature red"
/clone_id="KS05"
/note="Vector: pGEM-T easy; Site 1: EcoRI; SIRO red - SBV red suppression subtractive cDNA library of Hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."

BASE COUNT 96 a 59 c 108 t
ORIGIN

Alignment Scores:
Pred. No.: 3.62e-44 Length: 332
Score: 425.50 Matches: 81
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 1
Query Match: 95.62% Indels: 1
DB: 15 Gaps: 1

US-09-854-562-2 (1-83) x CB164858 (1-332)

QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
DB 78 ATGGCTGCTTCATTACTTACATGCAATTTCTGCTGGCAATGACCCCTTTGTTGCT 137
QY 20 TyrGlyValGlnGlyLysGlnIleCysCysLysGlnLeuThrLysProValLysCysSer 39
DB 138 TATGGGGTGAAGCAAGCAAAATTCTGCTGTAAGAAGCTCACAAAACCTGTAATATGTTCT 197
QY 40 SerAspProLeuCysGlnLysLeuCysMetGlnLysGlnLysTyrGlnLysGlyHisCys 59
DB 198 AGTACCCCTTATGTCATAAAACCTGTATGAGAAAGCAAAATATGAAGATGTCATTGT 257

QY 60 PheThrIleuSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 79
DB 258 TTCCACATCTTAAGCAAGATGCTTATGCAATGAGATGTAATGCTAAATCTTGGCAACA 317
QY 80 GlnLeuLeu 82
DB 318 GAATTGCTT 326

RESULT 6
BM064680 527 bp mRNA linear EST 11-SEP-2002
LOCUS BM064680
DEFINITION KS01070A06 KS01 Capsicum annuum cDNA, mRNA sequence.
ACCESSION BM064680
VERSION BM064680.1 GI:22784798
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 527)
Lee, S.-J., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G. and Choi, D.
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
JOURNAL Unpublished
COMMENT Contact: Doll Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doll@mail.krdb.re.kr
High quality sequence stop: 527.

FEATURES
Location/Qualifiers
1..527
/organism="Capsicum annuum"
/mol_type="mRNA"
/cultivar="Bukang"
/db_xref="taxon:4072"
/tissue_type="leaf inoculated with Xanthomonas campestris pv. glycines"
/dev_stage="8 weeks after germination"
/clone_id="KS01"
/note="Vector: pBluescript SK(-)"

BASE COUNT 175 a 74 c 100 g 178 t
ORIGIN

Alignment Scores:
Pred. No.: 6.69e-44 Length: 527
Score: 425.50 Matches: 81
Percent Similarity: 97.59% Conservative: 0
Best Local Similarity: 97.59% Mismatches: 1
Query Match: 95.62% Indels: 1
DB: 12 Gaps: 1

US-09-854-562-2 (1-83) x BM064680 (1-527)

QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
DB 31 ATGGCTGCTTCATTACTTACATGCAATTTCTGCTGGCAATGACCCCTTTGTTGCT 90
QY 20 TyrGlyValGlnGlyLysGlnIleCysCysLysGlnLeuThrLysProValLysCysSer 39
DB 91 TATGGGGTGAAGCAAGCAAAATTCTGCTGTAAGAAGCTCACAAAACCTGTAATATGTTCT 150
QY 40 SerAspProLeuCysGlnLysLeuCysMetGlnLysGlnLysTyrGlnLysGlyHisCys 59
DB 151 AGTACCCCTTATGTCATAAAACCTGTATGAGAAAGCAAAATATGAAGATGTCATTGT 210
QY 60 PheThrIleuSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 79

Db 211 TTACACATCTTACGAGAAAGCTTATGATGAGAAAGATCTTAATGCTTAACCTTCGACACA 270
 Oy 80 Glutuleu 82
 271 GAACCTGCTT 279

RESULT 7
 LOCUS CB185066 648 bp mRNA linear EST 03-FEB-2003
 DEFINITION KS04236770 KS04 Capsicum chinense cDNA, mRNA sequence.
 ACCESSION CB185066
 VERSION CB185066.1 GI:28197059
 KEYWORDS EST.
 SOURCE Capsicum chinense
 ORGANISM Capsicum chinense
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Capsicum.
 1 (bases 1 to 648)
 Lee,S.-J., Lee,M.-Y., Choi,S.-H., Her,N.-H., Yang,S.-G. and Harn,C.-H.
 Generation of Expressed Sequence Tags from Hot pepper (Capsicum
 chinense) and Sequence Analysis in Relation to Hypersensitive
 Response Against Pathogen
 Unpublished
 Contact: Chee Hark Harn
 Biotechnology center
 NONG WOOL BIO CO.,LTD.
 537-17 Jeongdan, Ganam, Yeosu, Kyonggi 469-885, Republic of Korea
 Tel: 82 31 883 7055
 Fax: 82 31 884 7065
 Email: charnongwoobio.co.kr
 Seq primer: T7.
 Location/Qualifiers
 1..648
 /organism="Capsicum chinense"
 /mol_type="mRNA"
 /cultivar="P1257284"
 /db_xref="taxon:80379"
 /sex="thermaphrodite"
 /tissue_type="leaf"
 /dev_stage="7-8 weeks-old leaves"
 /clone_11b="KS04"
 /note="Vector: pGEM-T easy; Site 1: EcoRI; PMWV-induced
 suppression subtractive cDNA library of Hot pepper. The
 subtraction was performed using the PCR-select cDNA
 subtraction kit (Clontech, Palo Alto, CA) according to the
 manufacturer's instructions. For a tester, cDNA from
 HR-developing pepper leaves (sampled after 3 days
 inoculation) was synthesized using AMV reverse
 transcriptase while, for a driver, cDNA from noninoculated
 pepper leaves was synthesized. After the subtractive
 hybridization, the subtracted cDNAs are selectively
 amplified by using nested PCR primers to enrich
 differentially expressed sequences."

BASE COUNT 197 a 115 c 132 g 196 t 8 others
 ORIGIN

Alignment Scores:
 Pred. No.: 8.82e-44 Length: 648
 Score: 425.50 Matches: 82
 Percent Similarity: 97.62% Conservative: 0
 Best local Similarity: 97.62% Mismatches: 1
 Query Match: 95.62% Indels: 1
 Gaps: 14

US-09-854-562-2 (1-83) x CB185066 (1-648)

Oy 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
 Db 132 ATGGCTGCTTCCATTACTTACATGCGATTTCTTGCTTGCGAAGACACCTTTGTTGCC 191
 Oy 20 TtyGlyValGlnGlyGlyGlnIleCysGlyGlyGlnLeuThrIleProValIleGlySer 39

Db 192 AATGGGAGTCAAGGACAGGAAATTTGCTGTAAGATCAAAAACCTGTAATATTTCT 251
 Oy 40 SerAspProLeuGlyGlnIleLeuGlySerGlnIleGlyGlnIleGlyGlnIleGlyGlnIle 59
 Db 252 AGTGAACCTCTATGTCATCAAAAACCTGATGAGAGAGAAATATGAAAGATGCTATTT 311
 Oy 60 PheThrIleLeuSerIleGlyGlnIleGlyGlnIleGlyGlnIleGlyGlnIleGlyGlnIle 79
 Db 312 TTACACATCTTACGAGAAAGCTTATGATGAGAAAGATGATGCTTAACCTTCGACACA 371
 Oy 80 GlutuleuAla 83
 372 GAATGCTTCTCT 383

RESULT 8
 LOCUS BM062133 530 bp mRNA linear EST 11-SEP-2002
 DEFINITION KS0103806 KS01 Capsicum annuum cDNA, mRNA sequence.
 ACCESSION BM062133
 VERSION BM062133.1 GI:22782251
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Capsicum.
 1 (bases 1 to 530)
 Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S.,
 Hur,C.-G. and Choi,D.
 Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
 annuum L.) and Sequence Analysis in Relation to Hypersensitive
 Response Against Pathogen
 Unpublished
 Contact: Dail Choi
 Genome Research Center and National Center for Genome Information
 Korea Research Institute of Bioscience and Biotechnology
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doilemail.kr@db.re.kr
 High quality sequence stop: 530.
 Location/Qualifiers
 1..530
 /organism="Capsicum annuum"
 /mol_type="mRNA"
 /cultivar="Bukang"
 /db_xref="taxon:4072"
 /tissue_type="leaf"
 /dev_stage="8 weeks after germination"
 /clone_11b="KS01"
 /note="Vector: pBluescript SK(-)"

BASE COUNT 176 a 76 c 99 g 179 t
 ORIGIN

Alignment Scores:
 Pred. No.: 7.81e-44 Length: 530
 Score: 425.00 Matches: 83
 Percent Similarity: 97.65% Conservative: 0
 Best local Similarity: 97.65% Mismatches: 0
 Query Match: 95.51% Indels: 2
 Gaps: 12

US-09-854-562-2 (1-83) x BM062133 (1-530)

Oy 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 20
 Db 34 ATGGCTGCTTCCATTACTTACATGCGATTTCTTGCTTGCGAAGACACCTTTGTTGCC 93
 Oy 20 TtyGlyValGlnGlyGlyGlnIleCysGlyGlyGlnLeuThrIleProValIleGlySer 40
 Db 94 ATGGGAGTCAAGGACAGGAAATTTGCTGTAAGATGCTCAAAAACCTGTAATATTTCT 153

Oy	40	expasprouleucysglnuysleucysmetglnuysglnuysrtyglnuapglvhsCysp	60
Db	154	GTACCCCTCTATGTCAAAAACCTCTGTATGCGAAGGAAATATGAAGATGGCTATTGT	213
Oy	60	hehrhrlleuseerlyscysleucysmetlysaagcysaenalaivsthrleuallatng	80
Db	214	TCACAAATCCAAAGCAAGCTCTATGATGAAAGATATATGCTAAACTTCGCAACAG	273
Oy	80	luleuleuAla	83
Db	274	ATTGCTGTCT	284
RESULT 9			
LOCUS	CB164824	496 bp	mRNA
DEFINITION	K805000310 K805 Capsicum annuum cDNA, mRNA sequence.		linear
ACCESSION	CB164824		
VERSION	CB164824.1		GI:28150950
KEYWORDS	EST.		
SOURCE	Capsicum annuum		
ORGANISM	Capsicum annuum		
REFERENCE	Bakayocra; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.		
AUTHORS	1 (bases 1 to 496)		
TITLE	Lee,S.J., Lee,M.Y., Lee,P.S., Choi,S.H. and Harn,C.H.		
JOURNAL	EST fragments generated by SSH of SIRO red - SBV red		
COMMENT	Unpublished		
	Contact: Chee Hark Harn		
	Biotechnology Center		
	NONG WOO Bldg CO., LTD.		
	537-17 Jeongdan, Ganam, Yeosu, Yeonggi 469-885, Republic of Korea		
	Tel: 82 31 883 7055		
	Fax: 82 31 884 7065		
	Email: chharn@nongwoobio.co.kr		
FEATURES	Seq primer: 77.		
source	Location/Qualifiers		
	1..496		
	/organism="Capsicum annuum"		
	/mol_type="mRNA"		
	/culti_var="SIRO, SBV"		
	/db_xref="taxon:4072"		
	/sex="hermaphrodite"		
	/tissue_type="fruit"		
	/dev_stage="mature red"		
	/clone_id="K805"		
	/note="Vector: pGEM-T easy; Site 1: EcoRI, SIRO red - SBV		
	red suppression subtractive cDNA library of Hot pepper.		
	The subtraction was performed using the PCR-select cDNA		
	subtraction kit (Clontech, Palo Alto, CA) according to the		
	manufacturer's instructions. For a tester, cDNA from		
	HR-developing pepper leaves sampled after 3 days		
	inoculation was synthesized using AMV reverse		
	transcriptase while, for a diver, cDNA from noninoculated		
	pepper leaves was synthesized. After the subtractive		
	hybridization, the subtracted cDNAs are selectively		
	amplified by using nested PCR primers to enrich		
	differentially expressed sequences."		
BASE COUNT	155 a	77 c	99 g
ORIGIN			165 t
Alignment Scores:			
Pred. No.:	1..496-43	Length:	496
Score:	422.50	Matches:	80
Percent Similarity:	97.59%	Conservative:	1
Best Local Similarity:	96.39%	Mismatches:	1
Query Match:	94.94%	Indels:	1
DB:	13	Gaps:	1
OS-09-854-562-2 (1-83) x CB164824 (1-496)			
Oy	1	MetAlaIGSerIleTyPheMetAlaPheUeuValLeuAla---	ThirLeuPheValAla 19

Db		69	ATGGCTCGTTCATTACTTACCTCATGCGCAATTTCTTGCTGTGGCAATGCACCTTTTGTCT	128
Oy		20	TYXGI,YVAIGLIGLYVGLIIECYaCYeLYeGILueThriLYseProVALyeCySeSer	39
Db		129	TATGGAGTCCAAAGCAGAGAAATTTGCTGTGAAGACTCACAAAACCTGTTAAATGTTCT	188
Oy		40	SerAPPrOLEuCYeGILuLYeLeuCYeMetGLuLYeGILuLYeTYrGLuApGLYhiSCYe	59
Db		189	AGTGAACCCCTTAATGCACAAAACTCTGTATGGAAGAAGAAATAATGAAATAGTCAATGT	248
Oy		60	PheThrIIleLeuSerLYeCYaLeuCYeMeLLyeAryCYeAsALaleThrDeuAlaThr	79
Db		249	TTCACATCTTAGAGNAAGTCTTATGCATGAAGAATGTAAATGCTTAAACTCTTGACA	308
Oy		80	GILueLeu 82	
Db		309	GAATTCCTT 317	
RESULT 10				
LOCUS		CB185076	720 bp	mRNA linear EST 03-FEB-2003
DEFINITION		KS04192170 KS04 Capsicum chinense cDNA, mRNA sequence.		
ACCESSION		CB185076		
VERSION		CB185076.1 GI:28197069		
KEYWORDS		EST.		
SOURCE		Capsicum chinense		
ORGANISM		Capsicum chinense		
REFERENCE		Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
TITLE		asterids; lamids; Solanales; Solanaceae; Capsicum.		
JOURNAL		Lee,S.J., Lee M.Y., Choi S.H., Her N.H., Yang S.G. and Harn,C.H.		
COMMENT		Genome and Expressed Sequence Tags from Hot pepper(Capsicum chinense) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen Unpublished		
CONTACT:		Chee Hark Harn		
BIOTECHNOLOGY CENTER		NONG WOOL BIO CO., LTD.		
TEL:		537-17 Jeongdan, Ganam, Yeosu, Kyonggi 469-885, Republic of Korea		
FAX:		82 31 881 7055		
EMAIL:		82 31 884 7065		
Seq primer:		chharmongwobio.co.kr		
Location/Qualifiers				
1..720				
/organism="Capsicum chinense"				
/mol_type="mRNA"				
/cultivar="P1257284"				
/db_xref="taxon:80379"				
/sex="hermaphrodite"				
/tissue_type="leaf"				
/dev_stage="7-8 weeks-old leaves"				
/clone_id="KS04"				
/note="Vector: pGEM-T easy; Site 1: EcoRI; PMW-induced suppression subtractive cDNA library of Hot pepper. The subtraction was performed using the PCR-select cDNA subtraction kit (Clontech, Palo Alto, CA) according to the manufacturer's instructions. For a tester, cDNA from HR-developing pepper leaves sampled after 3 days inoculation was synthesized using AMV reverse transcriptase while, for a driver, cDNA from noninoculated pepper leaves was synthesized. After the subtractive hybridization, the subtracted cDNAs are selectively amplified by using nested PCR primers to enrich differentially expressed sequences."				
BASE COUNT		203 a	114 c	133 g
ORIGIN				
Alignment Scores:				
Prod.No.:		3,28e-43	Length:	720
Score:		421.50	Matches:	81

Percent Similarity: 97.59%
 Best Local Similarity: 97.59%
 Query Match: 14
 Gaps: 11

US-09-854-562-2 (1-83) x CB185076 (1-720)

QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuA1a19
 DB 200 ATGGCTGCTTCATTAAGCAATTCCTGCTGCAATGACACTCTTGTGCT 259
 QY 20 TyrGlyValGlnGlyIleGlySerGlyGlyLeuThrIlePheValIleGlySer 39
 DB 260 AATGGGATGCAAGCAAGAAATTTGCTGTAAGAGCTCAAAAACCTGTTAAATGTTCT 319
 QY 40 SerAspProLeuGlyGlnIleGlySerGlyGlyLeuThrIlePheValIleGlySer 59
 DB 320 AGGACCTCTTAAGCAAGAAATTCCTGTAAGAGCAAGAAATGCAATGCTCATTTCT 379
 QY 60 PheThrIleLeuSerIleGlySerGlyGlyLeuThrIlePheValIleGlySer 79
 DB 380 TTCACATCTCTTAAGCAAGAGCTGTAAGAGCAAGAAATGCAATGCTCATTTCT 439
 QY 80 GluLeuLeu 82
 DB 440 GAATGCTN 448

RESULT 11
 AF082706 231 bp mRNA linear EST 27-MAR-2000
 LOCUS AF082706 Capsicum annuum leaf mRNA Capsicum annuum cDNA clone 12
 DEFINITION similar to gamma-chionin-like protein, mRNA sequence.
 ACCESSION AF082706 GI:3462809
 VERSION AF082706.1
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 231)
 Jung, H.W. and Hwang, B.K.
 Isolation, partial sequencing, and expression of pathogenesis-related cDNA genes from pepper leaves infected by Xanthomonas campestris pv. vesicatoria

1. Plant Microbe Interact. 13 (1), 136-142 (2000)

JOURNAL MEDLINE
 PUBMED 10656596
 CONTACT: Byung Kook Hwang
 Department of Agricultural Biology
 Korea University
 Anam-dong, Sungbuk-gu, Seoul 136-701, Korea
 Email: bkwang@kucn.korea.ac.kr.

FEATURES
 source location/Qualifiers
 1..231

/organism="Capsicum annuum"
 /mol_type="mRNA"
 /cultivar="Handyul"
 /db_xref="taxon:4072"
 /clone="12"
 /issue_type="leaf"
 /clone_lib="Capsicum annuum leaf mRNA"

BASE COUNT 70 a 38 c 45 g 78 t

ALIGNMENT SCORES:

Pred. No.: 3,7e-32 Length: 231
 Score: 329.50 Matches: 63
 Percent Similarity: 98.44% Conservative: 0
 Best Local Similarity: 98.44% Mismatches: 0
 Query Match: 74.04% Indels: 1
 Gaps: 9

US-09-854-562-2 (1-83) x AF082706 (1-231)

QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuA1a19
 DB 40 ATGGCTGCTTCATTAAGCAATTCCTGCTGCAATGACACTCTTGTGCT 99
 QY 20 TyrGlyValGlnGlyIleGlySerGlyGlyLeuThrIlePheValIleGlySer 39
 DB 100 TATGGGATGCAAGCAAGAAATTTGCTGTAAGAGCTCAAAAACCTGTTAAATGTTCT 159
 QY 40 SerAspProLeuGlyGlnIleGlySerGlyGlyLeuThrIlePheValIleGlySer 59
 DB 160 AGTACCTCTTAAGCAAGAAATTCCTGTAAGAGCAAGAAATGCAATGCTCATTTCT 219
 QY 60 PheThrIleLeu 63
 DB 220 TTCACATCTCTTA 231

RESULT 12
 CA524161 521 bp mRNA linear EST 15-NOV-2002
 LOCUS K512033604 K512 Capsicum annuum cDNA, mRNA sequence.
 DEFINITION CA524161
 ACCESSION CA524161 GI:25038231
 VERSION CA524161.1
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 521)
 Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G. and Choi, D.
 Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen

1. Unpublished
 CONTACT: Doil Choi
 Genome Research Center and National Center for Genome Information
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doil@mail.kribb.re.kr
 Plate: 033 row: G column: 04.

FEATURES
 source location/Qualifiers
 1..521

/organism="Capsicum annuum"
 /mol_type="mRNA"
 /db_xref="taxon:4072"
 /clone_lib="K512"

BASE COUNT 163 a 77 c 101 g 180 t

ALIGNMENT SCORES:

Pred. No.: 1.09e-31 Length: 521
 Score: 329.50 Matches: 63
 Percent Similarity: 85.23% Conservative: 12
 Best Local Similarity: 71.59% Mismatches: 8
 Query Match: 74.04% Indels: 5
 DB: 14 Gaps: 2

US-09-854-562-2 (1-83) x CA524161 (1-521)

QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuA1a19
 DB 56 ATGGCTGCTTCATTAAGCAATTCCTGCTGCAATGACACTCTTGTGCT 115
 QY 20 TyrGlyValGlnGlyIleGlySerGlyGlyLeuThrIlePheValIleGlySer 39
 DB 116 AATGGGATGCAAGCAAGAAATTTGCTGTAAGAGCTCAAAAACCTGTTAAATGTTCT 175
 QY 40 SerAspProLeuGlyGlnIleGlySerGlyGlyLeuThrIlePheValIleGlySer 59

```

Db 176 AGTACCGGCTATGTCAACAAATCTGTATTAAGAGGAGAACTTGAAGATGTCATGCT 235
Qy 60 PheThrlleuSerlyCySeuCyMetlybArgCySasn-----AlalyS 75
Db 236 TTCAACATCTTCAAGAGAGTGCATGTCATGAGAGATGTAATGTGTTCAAGATGTTAA 295
Qy 76 ThrlleuAlaThrlleuLeuAla 83
Db 296 ACTCTCCAGCAAAATGCTTCT 319

RESULT 13
LOCUS BM062737 535 bp mRNA linear EST 11-SEP-2002
DEFINITION KS01046F09 KS01 Capsicum annuum cDNA, mRNA sequence.
ACCESSION BM062737
VERSION BM062737.1 GI:22782855
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 535)
AUTHORS Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S.,
Hur,C.-G. and Choi,D.
TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen
JOURNAL Unpublished
COMMENT Contact: Doil Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doilemail.kr@db.re.kr
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Db 93 AATGAGTGGAGAGGTAAGAAATTTGCTGTAAAGATGCTCAAGAGCTTATATGTTCT 152
Qy 40 SerAspProLeuCySeuGluylsLeuCyMetGluylsGluylsTyrgluAepGlyHlaCyS 59
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Qy 76 ThrlleuAlaThrlleuLeuAla 83
Db 273 ACTCTCCAGCAAAATGCTTCT 296

RESULT 14
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VERSION BM063527.1 GI:22783645
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SOURCE Capsicum annuum
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asterids; lamiales; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 540)
AUTHORS Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S.,
Hur,C.-G. and Choi,D.
TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen
JOURNAL Unpublished
COMMENT Contact: Doil Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doilemail.kr@db.re.kr
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Query Match: 74.04% Indels: 5
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Qy 20 TyrglyValgInglyLygGluileCySeuCySlysguLeuThrllySProvallySvSser 39
Db 99 AATGAGTGGAGAGGTAAGAAATTTGCTGTAAAGATGCTCAAGAGCTTATATGTTCT 158
Qy 40 SerAspProLeuCySeuGluylsLeuCyMetGluylsGluylsTyrgluAepGlyHlaCyS 59
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Db 219 TTACACATCTTAAGGAGGCGTATGCAATGAGAGATGTAATGTGTTACAGATGTTAA 278
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CA525505

LOCUS CA525505 545 bp mRNA linear EST 15-NOV-2002

DEFINITION KS1205607 KS12 Capsicum annum CDNA, mRNA sequence.

ACCESSION CA525505

VERSION CA525505.1 GI:25039585

KEYWORDS EST.

SOURCE Capsicum annum

ORGANISM Capsicum annum

Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 545)

AUTHORS Lee,S.-Y., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pal,H.-S.,

Hur,C.-G., and Choi,D.

Generation of Expressed Sequence Tags from Hot Pepper (Capsicum

annuum L.) and Sequence Analysis in Relation to Hypersensitive

Response Against Pathogen

Unpublished

CONTACT: Doh Choi

Genome Research Center and National Center for Genome Information

Korea Research Institute of Bioscience and Biotechnology

P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea

Tel: 82-42-860-4340

Fax: 82-42-860-4309

Email: doil@mail.kribd.re.kr

Plate: 056 row: G column: 07.

Location/Qualifiers

FEATURES

source

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Score: 1.16e-31

Percent Similarity: 329.50

Best Local Similarity: 85.23%

Query Match: 74.04%

DB: 14

Length: 545

Matches: 63

Conservative: 12

Mismatches: 8

Indels: 5

Gaps: 2

US-09-854-562-2 (1-83) x CA525505 (1-545)

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Qy 20 TyrgIyAlaIngIlysgIuIeCySylsgIuLeuThrlYsProValIysCySer 39

Db 110 AATGAGGTGCAAGGTATAGGAAATTGCTGTAAAGATGTCACAGAGCTGTATATATGTTCT 169

Qy 40 SerAspProLeuCySgInIysLeuCySmetGluIysIyTyrgIuAspGlyHisCys 59

Db 170 AGTGACCCGCTATGTAAACAATCTGTATCGAAGAGGAACTATGAAGATGTCATGT 229

Qy 60 PheThrlleuSerIysCySleuCySmetIysAlaGlyCysAen-----AlaIys 75

Db 230 TTCACATCTTAAGGAGGCGTATGCAATGAGAGATGTATGTGTTACAGATGTTAA 289

Qy 76 ThrlauAlathrgluLeuAla 83

Db 290 ACTCTCGCAGCAAAATGCTTCT 313

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model.

Run on: August 23 2003, 06:31:08 ; Search time 2024 Seconds

(without alignments)
1677.618 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0
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Searched: 288671 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	434.5	97.6	506	8	AF112443 Capsicum
2	431.5	97.0	548	8	AF112869 Capsicum
3	234	52.6	559	8	AF128239 Capsicum
4	189.5	42.6	558	8	AB005266 Nicotiana
5	188	42.2	601	8	AF509566 Nicotiana
6	186	41.8	589	8	SFSTWRNA
7	182.5	41.0	596	8	SLU20591
8	177.5	39.9	549	8	AB005250 Lyc
9	156	35.1	448	8	AB005265 Nicotiana
10	130.5	29.3	456	8	AF507975 Nicotiana
11	129	29.0	602	8	AF507976 Nicotiana
12	94.5	21.2	470	8	ST322R
13	90.5	20.3	139934	8	AP003272 Oryza sat
14	90.5	20.3	178649	8	AP003246 Oryza sat
15	89	20.0	382	8	AB052687
16	88.5	19.9	242507	2	AC134246 Mus muscu
17	87.5	19.7	177202	2	AC118703 Mus muscu
18	87	19.6	401	8	AB052689 Pyrus pyr
19	87	19.6	181376	2	AC114990 Mus muscu
20	87	19.6	238725	2	AC130214 Mus muscu
21	86.5	19.4	527	8	GMU12150 Glycine max
22	84.5	19.0	403	8	OSU72942 Oryza sativ
23	84.5	19.0	458	8	AB052688 Pyrus pyr
24	84.5	19.0	63748	8	AP000604 Arabidops
25	84	18.9	594	8	AB085469 Arabidops
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27	84	18.9	594	6	AR170812 Sequence
28	84	18.9	109155	8	ATT20K12 Arabidops
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33	83.5	18.8	179115	9	AP004710 Homo sapi
34	83	18.7	2608	10	AF373288 Mus muscu
35	83	18.7	171287	2	AC131115 Mus muscu
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38	82.5	18.5	255654	2	AC107481 Rattus no
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40	82	18.4	188095	4	AC091505 Sus scro
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RESULT 1

ALIGNMENTS

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 ORGANISM Capsicum annuum
 Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 506)
 AUTHORS Oh, B.J., Ko, M.K., Koestenyuk, I., Shin, B. and Kim, K.S.
 TITLE Coexpression of a defense gene and a thionin-like via different signal transduction pathways in pepper and Colletotrichum gloeosporioides interactions
 JOURNAL Plant Mol. Biol. 41 (3), 313-319 (1999)
 MEDLINE 20064969
 PUBMED 10598099
 REFERENCE 2 (bases 1 to 506)
 AUTHORS Oh, B.J., Ko, M.K., Koestenyuk, I.A., Shin, B.C. and Kim, K.S.
 TITLE Direct Submission
 JOURNAL Submitted (09-DEC-1998) Kumho Life and Environmental Science Laboratory, Kumho Petrochemical Co., Ltd., 1 Oryong-dong, Puk-gu, Kwangju 500-712, Korea
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RESULT 2
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 LOCUS AF112869
 DEFINITION Capsicum annuum gamma-thionin 1 precursor (thion1) mRNA, complete cds.
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 VERSION AF112869.1 GI:6601330
 KEYWORDS
 ORGANISM Capsicum annuum
 Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 548)
 AUTHORS Hwang, B.K., Lee, S.C., Kim, Y.J. and Hong, J.K.
 TITLE Molecular cloning and pathogen-induced expression of a thionin gene in pepper plants
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 548)
 AUTHORS Hwang, B.K., Lee, S.C., Kim, Y.J. and Hong, J.K.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-1998) Dept. of Agricultural Biology, Korea University, Anam-dong, Sungbuk-gu, Seoul 136-701, Korea
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 Db 172 AGTGACCTCTATGTCAAAACTGTATGAGAGAGAAATATGAGATGCTCATTTCT 231
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Db      232 TTCACATCTTCAAGAGAGTGTATGATGATGAAGAGATGATTAATCTAAACTCCGACAA 291
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DEFINITION Capsicum chinense putative gamma-chionin precursor, mRNA, complete cds.
ACCESSION AF128239
VERSION   AF128239.1 GI:4457222
KEYWORDS
SOURCE    Capsicum chinense
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; lamiales; Solanales; Solanaceae; Capsicum.
REFERENCE
AUTHORS  Aluru,M., Curry,U. and O'Connell,M.A.
TITLE     Nucleotide sequence of a defensin or gamma-chionin-like gene
            (Accession No. AF128239) from habanero chile (PGR 99-070)
JOURNAL   Plant Physiol. 120 (2), 633 (1999)
REFERENCE
AUTHORS  Curry,U., Aluru,M. and O'Connell,M.A.
TITLE     Direct Submission
JOURNAL   Submitted (12-FEB-1999) Agronomy and Horticulture, New Mexico State
            University, P.O. Box 30003, MSC 3Q, Las Cruces, NM 88003, USA

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Score: 234.00
Percent Similarity: 63.00%
Best Local Similarity: 50.00%
Query Match: 52.58%
Length: 559
Matches: 50
Conservative: 13
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Indels: 18
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Qy      38 CysSerSerAspProLeuCysGlnLysLeuCysMetGluLysGluLysTyRgluAspGly 57
Db      159 TGTTTTGCGACTTAATGTGAAAGATTGTATCCAGAGGATTAATTTGAAGATGT 218
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DEFINITION Nicotiana excelsior mRNA for gamma-chionin, complete cds.
ACCESSION AB005266
VERSION   AB005266.1 GI:2244704
KEYWORDS  gamma-chionin.
SOURCE    Nicotiana excelsior
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS  Yamada,S., Komori,T. and Imaseki,H.
TITLE     1 (sites)
            CDNA cloning of gamma-chionin from Nicotiana excelsior (Accession
            No. AB005266) (PGR97-131)
JOURNAL   Plant Physiol. 115, 314 (1997)
REFERENCE
AUTHORS  Yamada,S.
TITLE     2 (bases 1 to 558)
JOURNAL   Direct Submission
            Submitted (26-JUN-1997) Shigehiro Yamada, Plant Breeding and
            Genetics Research Laboratory, Japan Tobacco Inc., 700 Higashibara,
            Iwata, Shizuoka 438, Japan
            (E-mail:Shigehiro.Yamada@jtbl.co.jp, Tel:0538-32-7116,
            Fax:0538-32-8700)

FEATURES
source    1..558
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            /organism="Nicotiana excelsior"
            /mol_type="mRNA"
            /db_xref="taxon:61185"
            1..558
            /gene="Nethio2"
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            /gene="Nethio2"
            /codon_start=1
            /product="gamma-chionin"
            /protein_id="BA021114.1"
            /db_xref="GI:2244705"
            /translation="MARSVCFMAFALIAVLAFLVAVDVEAKDKTESNTPPGICITKPP
            CRKACIKKFKFDGHSKILRRCLCTKRCVDEKMIKTAETLAETTLAALLLEEI
            MN"

BASE COUNT 170 a 94 c 108 g 186 t
ORIGIN
Alignment Scores:
Pred. No.: 6.97e-15
Score: 189.50
Percent Similarity: 60.00%
Best Local Similarity: 47.78%
Query Match: 42.58%
Length: 558
Matches: 43
Conservative: 11
Mismatch: 25
Indels: 11
Gaps: 3

US-09-854-562-2 (1-83) x AB005266 (1-558)
Qy      1 MetAlaArgSerIleTyRPhMetAlaPheLeuValIleuAlaThr---LeuPheValAla 19
Db      33 ATGGCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 92
Qy      20 TYRGLVAlGInGLyLysGluIleCysCysLysGluLeuThrLysProValLysCysSer 39
Db      93 TATGATGTGAAGCTTAAGATTTGCAAAACGAAAGCAATTCATTCCTGGAATATGCAATT 152
Qy      40 SerAspProLeuCysGlnLysLeuCysMetGluLysGluLysTyRgluAspGly 59
Db      153 ACCAAACACACATGACGAGAAAGCTTGTATC---AAGAGAAATTAATGATGCTCATGTT 209
Qy      60 PheThrIleLeuSerLysCysLeuCysMetLysArgCys----- 72

```

Db 210 AGCAAAATCCTGAGAGGTGTCTATGACTAAGCATGTGTGTTGATGAGAAATGATGC 269

Qy 73 -----AsnAlaIysThrIleuAlaThrGlu 80
 |||:::|||||
 Db 270 AAAACAGAGCTGAACCTTACTGATGAGAA 299

RESULT 5
 AF509566 601 bp mRNA linear PLN 19-MAR-2003
 LOCUS Nicotiana glauca flower-specific defensin precursor (Nad1) mRNA,
 DEFINITION complete cds.
 ACCESSION AF509566
 VERSION AF509566.1 GI:25005096
 KEYWORDS
 SOURCE Nicotiana glauca (Persian tobacco)
 ORGANISM Nicotiana glauca
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
 REFERENCE 1 (bases 1 to 601)
 Lay,F.T., Schirra,H.J., Scanlon,M.J., Anderson,M.A. and Craik,D.J.
 TITLE The three-dimensional solution structure of Nad1, a new floral
 defensin from Nicotiana glauca and its application to a homology
 model of the crop defense protein alfap
 J. Mol. Biol. 325 (1), 175-188 (2003)
 JOURNAL MEDLINE 22361678
 PUBMED 12473460
 REFERENCE 2 (bases 1 to 601)
 Lay,F.T., Brugliera,F. and Anderson,M.A.
 TITLE Isolation and Properties of Floral Defensins from Ornamental
 Tobacco and Petunia
 Plant Physiol. 131 (3), 1283-1293 (2003)
 JOURNAL PUBMED 12644678
 REFERENCE 3 (bases 1 to 601)
 Lay,F.T. and Anderson,M.A.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-2002) Biochemistry, La Trobe University,
 Bundoora, VIC 3086, Australia
 FEATURES
 source
 1..601
 /location/Qualifiers
 /organism="Nicotiana glauca"
 /mol_type="mRNA"
 /db_xref="taxon:4087"
 1..601
 /gene="Nad1"
 61..378
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 /note="Nad1, gamma-thionin, possesses antifungal activity;
 targeted to the vacuole"
 /codon_start=1
 /product="flower-specific defensin precursor"
 /protein_id="AAW70999.1"
 /db_xref="GI:25005097"
 /translation="MASSLCFMAFALLAMLFAYVQARCKTSNPPGICITKPP
 CRKACISKFTDGHGSKILRCLCTKCVDFDKMTKTAETLVBAKTLAALLLEEEI
 MDN"
 mat_peptide
 136..276
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 /product="flower-specific defensin"
 BASE COUNT 192 a 95 c 115 g 199 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,17e-14 Length: 601
 Score: 188.00 Matches: 45
 Percent Similarity: 54.55% Conservative: 9
 Best Local Similarity: 45.45% Mismatches: 27
 Query Match: 42.25% Indels: 18
 Gaps: 3
 DB: 8
 US-09-854-562-2 (1-83) x AF509566 (1-601)
 Qy 1 MetaIaArgSerIleTyrPheMetAlaPheLeuValIleuAla---ThrIleuPheValAla 19

Db 61 ATGGCTGCTGCTTGTGTGCTTTCATGACATTTGCGATATGCGCAATGATGCTCTTTTGGC 120
 |||:::|||||
 Qy 20 TYRGLValAlngInGlyLysGluIleCysValGluIleThrIlePheProValIleCysSer 39
 |||:::|||||
 Db 121 TATGAGTGCACGCTGAGGAAATGCAAAACGACACCATTTCTGGAATATGCAATT 180
 |||:::|||||
 Qy 40 SerAspProLeuCysGlnIleCysMetGluIleGluIleValIleGluIleValIleCys 59
 |||:::|||||
 Db 181 ACCAAACCAACCATGAGAAAGCTTGTATC---AGTAGAAATTTACTGATGCTCATTTGT 237
 |||:::|||||
 Qy 60 PheThrIleLeuSerLysCysLeuCysMetLysAspCys----- 72
 |||:::|||||
 Db 238 AGCAAAATCCTGAGAGGTGTCTATGACTAAGCATGTGTGTTGATGAGAAATGACT 297
 |||:::|||||
 Qy 73 -----AsnAlaIysThrIleuAlaThrGluIleu 82
 |||:::|||||
 Db 298 AAAACAGAGCTGAATTTTGGCTGAGAGCAAAACCTTGGCTGACATTTGCTT 354
 |||:::|||||

RESULT 6
 SPSMRNA 589 bp mRNA linear PLN 03-DEC-1993
 LOCUS Solanaceae mRNA for flower-specific thionin.
 DEFINITION 211748 S41631
 ACCESSION 211748.1 GI:21212
 VERSION
 KEYWORDS thionin.
 SOURCE Solanaceae
 ORGANISM Solanaceae
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamids; Solanales.
 REFERENCE 1 (bases 1 to 589)
 Gu,Q., Kawata,E.E., Morse,M.J., Wu,H.M. and Cheung,A.Y.
 TITLE A flower-specific cDNA encoding a novel thionin in tobacco
 JOURNAL Mol. Gen. Genet. 234 (1), 89-96 (1992)
 MEDLINE 92357021
 PUBMED 1495489
 REFERENCE 2 (bases 1 to 589)
 Gu,Q.
 TITLE Direct Submission
 JOURNAL Submitted (25-FEB-1992) Qing GU, Department of Biology, Yale
 University, 165 Prospect St, New Haven, CT, 06511, USA
 FEATURES
 source
 1..589
 /organism="Solanaceae"
 /mol_type="mRNA"
 /db_xref="taxon:4070"
 /clone="49a"
 /tissue_type="flower of tobacco"
 /dev_stage="flowering"
 49..366
 /codon_start=1
 /product="flower-specific thionin"
 /protein_id="CAA77806.1"
 /db_xref="GI:21213"
 /db_xref="SUNIS-PROT:P32026"
 /translation="MASSLCFMAFALLAMLFAYVQARCKTSNPPGICITKPP
 CRKACISKFTDGHGSKILRCLCTKCVDFDKMTKTAETLVBAKTLAALLLEEEI
 MDN"
 CDS
 49..366
 /product="flower-specific thionin"
 BASE COUNT 184 a 97 c 114 g 194 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.06e-14 Length: 589
 Score: 186.00 Matches: 44
 Percent Similarity: 54.55% Conservative: 10
 Best Local Similarity: 44.44% Mismatches: 27
 Query Match: 41.80% Indels: 18
 Gaps: 3
 DB: 8
 US-09-854-562-2 (1-83) x SPSMRNA (1-589)
 Qy 1 MetaIaArgSerIleTyrPheMetAlaPheLeuValIleuAla---ThrIleuPheValAla 19

Field	Value
Ref. No.:	5,84e-14
Score:	182.50
Percent Similarity:	62.35%
Best Local Similarity:	48.24%
Query Match:	41.01%
DB:	8
Length:	596
Matches:	41
Conservative:	12
Mismatches:	29
Indels:	3
Gaps:	3

US-09-854-562-2 (1-83) x SLU20591 (1-596)

Accession	Gene	Protein	Length	Score	Percent Similarity	Best Local Similarity	Query Match
1	MeA1AAGSelleTyPhemeA1A	PhleuValLeuA1A	19	182.50	62.35%	48.24%	41.01%
57	ATGCGTCGTCATTTCTTATGAGCAATTTTGGCTTCTTGCAATGACTCTTGTTC	116					
20	TyGlyValGInGlyLysGluLeuCs	--CysLysGluLeuThrLysProValLysCs	38				
117	TATGAGGTGAAGCTCCACCAATTTGGCAAGCCAAAGCAAACTTCCACAGATTAATGT	176					
39	SetSerAspProLeuCysGlnLysLeuCysMetGlnLysGlnLysTyGlnAspLys	58					
177	TTTATGAGTCACTCATGTAAGAAATATTGATC	--AAAGAGAAATTATCTGCTGGACAT	233				
59	CysPheThrIleLeuSerLysCysLeuCysMetLysArgCysAsnAlaLysThrLeuA	78					
234	TGTAGCAACTCCAAAGAGAAAGTCTATGACTATGACATGATGTAATTGACAAATCTCA	293					
79	ThrGlnLeuLeuA1A	83					
294	AGTGAAGTTAAAGCA	308					

RESULT 8

AB005250

Nicotiana paniculata mRNA for gamma-thionin, complete cds.

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AB005250.1 GI:2251080

gamma-thionin.

Nicotiana paniculata

Nicotiana paniculata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Nicotiana.

1 (sites)

Komori,T., Yamada,S. and Imaseki,H.

A cDNA clone for gamma-thionin from Nicotiana paniculata (Accession No. AB005250) (Per97-112)

Plant Physiol. 115, 314 (1997)

2 (bases 1 to 549)

Komori,T.

Direct Submission

Submitted (26-JUN-1997) Toshituki Komori, Plant Breeding and Genetics Research Laboratory, Japan Tobacco Inc., 700 Higashibara, Iwate, Shitnaka 438, Japan

(E-mail:Toshituki.Komori@pjgrl.jti.co.jp, Tel:0538-32-7116, Fax:0538-32-8700)

Location/Qualifiers

1..549

/organism="Nicotiana paniculata"

/mol_type="mRNA"

/db_xref="taxon:62141"

1..549

/gene="NpThiol"

48..368

/gene="NpThiol"

/codon_start=1

/product="gamma-thionin"

/protein_id="BA21325.1"

/db_xref="GI:2251081"

/translation="MARSLCPMAFAVLAMLLFAAYVQAKSTCKASNTFPGLCITKRPKRXCKLEKFTDCKSKILIRCIYKPCVPGFQKIQIGIAENLAENATLAAALLEBEMNDN"

BASE COUNT

166 a 87 c 112 g 184 t

ORIGIN

Alignment Scores:

Pred. No.: 2,33e-13 Length: 549
 Score: 177.50 Matches: 45
 Percent Similarity: 53.00% Conservative: 8
 Best Local Similarity: 45.00% Mismatches: 28
 Query Match: 39.89% Indels: 19
 DB: 8 Gaps: 4

US-09-854-562-2 (1-83) x AB005250 (1-549)

Oy 1 MetAlaArgSerIleYrPheMeAlaPheLeuValLeuAla---ThrLeuPheValAla 19
 Db 48 ATGGCTCCCTCCCTGCTTCATGCGCATTTGCGATTCGCGAAGAGCTTTTGTGCC 107
 Oy 20 TyrgIValGInGlyLeuGluIleCySeCySyluLeu---ThrlsPProVallySyls 38
 Db 108 TATGAGGTGCAAGCTAAGAGTACTTGCAAGACAGAAAGCATATCATTCCTCGATTATCC 167
 Oy 39 SerSerAspProLeuCySeGInlyLeuCySeMetCyluLeuGlyLeuTyrgIuaPpGlyHls 58
 Db 168 ATTAACCAACCAACCAATGCAAGAAAGCTTGTCTC---AGTGAAGAAATTACTGATGAAAA 224
 Oy 59 CySePheThrIleLeuSerlyCySeLeuCySeMetlySargCyS----- 72
 Db 225 TGTAGCAAAATCTCAGAGGTGCTATTGCTAACAGCCATGTGTATTGATGCAAGAGATG 284
 Oy 73 -----AenAlaYrThrLeuAlaThrGluLeu 82
 Db 285 ATCCAAACAGAGCTGAATAATTGGCCGACAGAGAGAAAGAACTTGGCTGACGCTTGCTT 344

RESULT 9

AB005265 448 bp mRNA linear PLN 04-JUL-1997
 LOCUS Nicotiana excelsior mRNA for gamma-thionin, partial cds.
 DEFINITION
 AB005265.1 GI:2244702
 VERSION gamma-thionin.
 KEYWORDS
 ORGANISM Nicotiana excelsior
 Nicotiana excelsior
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.

REFERENCE 1 (bases 1 to 448)
 Yamaoka, S., Komori, T. and Imaseki, H.
 cDNA cloning of gamma-thionin from Nicotiana excelsior
 JOURNAL Unpublished
 TITLE 2 (bases 1 to 448)
 AUTHORS Yamaoka, S.
 JOURNAL Direct Submission
 TITLE Submitted (26-JUN-1997) Shigehiro Yamada, Plant Breeding and
 Genetic Research Laboratory, Japan Tobacco Inc., 700 Higashibara,
 Iwata, Shizuoka 438, Japan
 (E-mail:Shigehiro.Yamada@pbgrl.jti.co.jp, Tel:0538-32-7116,
 Fax:0538-32-8700)

FEATURES

source location/Qualifiers
 1..448
 /organism="Nicotiana excelsior"
 /mol_type="mRNA"
 /db_xref="taxon:61185"
 1..448
 /gene="NetH101"
 <1..240
 /gene="NetH101"
 /product="gamma-thionin"
 /protein_id="BAA2113.1"
 /db_xref="GI:2244703"
 /translation="LFAVAVQARCAKEIFPTICITNPOCRKAKICEKFTDGHCKSI
 LRRCLCTKCTGAEATTAEEATTAALIEEIMDN"

CDS

gene
 141 a 73 c 88 g 146 t

BASE COUNT

Alignment Scores:

Pred. No.: 1.04e-10 Length: 448
 Score: 156.00 Matches: 34
 Percent Similarity: 68.18% Conservative: 11
 Best Local Similarity: 51.52% Mismatches: 17
 Query Match: 35.06% Indels: 4
 DB: 8 Gaps: 4

US-09-854-562-2 (1-83) x AB005265 (1-448)

Oy 16 LeuPheValAlaTyrgIValGInGlyLeuGluIleCySeCySyluLeuThrlySylsPro 35
 Db 1 CTTCTTTGTTGCTTATGAGGTGCTCAAGAGAA---TGCGCAAGAAATTTTCACTGGA 57
 Oy 36 VallyCySeSerSerAspProLeuCySeGInlyLeuCySeMetCyluLeuGlyLeuTyrgI 55
 Db 58 CTA---TGATTATCCAAATCCAAATGCAAGAAAGCTTGTATC---AAAGAAATTTACT 111
 Oy 56 AspGlyHlsCySePheThrIleLeuSerlyCySeLeuCySeMetlySargCyS---AenAla 74
 Db 112 GATGGTCATTGAGCAAAATCTCAGAGGTGCTATTGCACTAAGCATGACAGAGACT 171
 Oy 75 TyrThrLeuAlaThrGlu 80
 Db 172 GAACCTTAGCTGAGGAA 189

RESULT 10

AF507975 456 bp mRNA linear PLN 19-MAR-2003
 LOCUS Petunia x hybrida floral defensin-like protein 1 (D1) mRNA,
 DEFINITION complete cds.
 AF507975.1 GI:24817407
 VERSION Petunia x hybrida
 KEYWORDS
 SOURCE Petunia x hybrida
 ORGANISM Petunia x hybrida
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamiales; Solanales; Solanaceae; Petunia.

REFERENCE 1 (bases 1 to 456)
 Lay, F.T., Brugliera, F. and Anderson, M.A.
 Isolation and Properties of Floral Defensins from Ornamental
 Tobacco and Petunia
 JOURNAL Plant Physiol. 131 (3), 1283-1293 (2003)
 PUBMED 12644678

REFERENCE 2 (bases 1 to 456)
 Brugliera, F., Holton, T.A., Stevenson, T. and Mason, J.G.
 Direct Submission
 TITLE Submitted (30-APR-2002) Florigene Ltd, 16 Glpps St., Collingwood,
 Melbourne, Victoria 3066, Australia
 JOURNAL Location/Qualifiers
 1..456
 /organism="Petunia x hybrida"
 /mol_type="mRNA"
 /cultivar="Old Glory Blue"
 /db_xref="taxon:4102"

FEATURES

source location/Qualifiers
 1..456
 /gene="D1"
 /note="Phd1"
 68..379
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 /codon_start=1
 /product="floral defensin-like protein 1"
 /protein_id="AAAG4750.1"
 /db_xref="GI:24817408"
 /translation="MARSICFPYVALIAMLPRAYDAEAAATKACPTDSCVINKRP
 CVACKRAKESDGHCKILRRCLCTKCEVCFEKETATQETFTKDVNTIALALEADMM
 V"

CDS

gene
 124 a 92 c 102 g 138 t

BASE COUNT

Alignment Scores:

Pred. No.: 1.9e-07 Length: 456
 Score: 130.50 Matches: 36

BASE COUNT 126 a 70 c 100 g 174 t /note="polyma site"

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
0.0077	94.50	46.588	31.518	21.248	8
Length:	Matches:	Conservative:	Mismatch:	Indels:	Gaps:
470	23	11	32	7	3

US-09-854-562-2 (1-83) x ST322R (1-470)

Oy 6 TyrPheMetclaphleuValleualathrlleupheValalathrlGlyValGlnGlyLys 25
 Db 13 TTCTTGTCTACTTCTTCTTCTTCTTGTAGTATGCTTGTGCGGCTACTTAAGATGACCAATG 72
 Oy 26 GluIleCys-----CysLysGlnLeuThrLysProValLys-----CysSer 39
 Db 73 AGAATTCCAGAGCCAGACATTGCGAGTGTGAGCCATGCTTTCAAGGAGACCATGATGAC 132
 Oy 40 SerAspProLeuCysGlnLysLeuCysMetGlnLysGlnLysTrpGluAspGlyHisCys 59
 Db 133 AGAAGATAGCAATTTGCTCTTGGTCTGT---GAGACCGCAAAATTTTCGGTGGCAATTC 189
 Oy 60 PheThrIleLeuSerLysCysLeuCysMetLysAspGys 72
 Db 190 CATGATTCGCTGCGCGCTTCTTTGCTTGTCACTAAGCATTC 228

RESULT 13
 AP003272 139934 bp DNA linear PLN 29-MAR-2001
 LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
 DEFINITION PAC clone: P0506E04.
 ACCESSION AP003272 BAO00010
 VERSION AP003272.3 GI:15628365
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 KEYWORDS Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eumetridiidae; Oryzae; Oryza.

REFERENCE
 1 Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,
 Katsuyose, Y., Wu, J., Nishimura, Y., Cheng, Z., Nagamura, Y.,
 Antonio, B.A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,
 Chinden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Arita, K.,
 Hamada, M., Harada, C., Hijishita, S., Honda, M., Ichikawa, Y.,
 Idonuma, A., Iijima, M., Ikeda, M., Ikeno, M., Itoh, S., Itoh, T.,
 Itoh, Y., Itoh, Y., Iwabuchi, A., Kamiya, K., Karsawa, W., Katagiri, S.,
 Kikuta, A., Kobayashi, N., Kono, I., Machida, K., Maehara, T.,
 Mizuno, H., Mizubayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M.,
 Nakama, Y., Nakemichi, Y., Nakamura, M., Namiki, N., Negishi, M.,
 Ohta, I., Ono, N., Saji, S., Sakai, K., Shiba, M., Shimokawa, T.,
 Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Teuiji, K., Maki, K.,
 Yamagata, H., Yamane, H., Yoshiki, S., Yoshikawa, R., Yukawa, K.,
 Zhong, H., Iwama, H., Endo, T., Ito, H., Hama, J. H., Kim, H. I., Eun, M. Y.,
 Yano, M., Jiang, J. and Gojobori, T.
 The genome sequence and structure of rice chromosome 1
 Nature 420 (6913), 312-316 (2002)

TITLE
 JOURNAL MEDLINE
 PUBMED 12447438
 2 (bases 1 to 139934)
 Sasaki, T., Matsumoto, T. and Yamamoto, K.
 Direct Submission
 Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
 Agricultural Sciences, Rice Genome Research Program, Kannondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
 Tel:81-298-38-7441, Fax:81-298-38-7468
 On Sep 14, 2001, this sequence version replaced gi:15216345.
 Genes were predicted from the integrated results of the following:

GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1996 version). The genomic sequence was searched against NCBI Nonredundant Protein database, nr (<ftp://ncbi.nlm.nih.gov/blast/db>) and the cDNA sequence database at RGP. Protein homologues of the coding regions were searched against NCBI Nonredundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLAST2.0 with the corresponding DBS accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein. The orientation of the sequence is from SP6 to T7 of the PAC clone. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/GenomeSeq.html>.

location/Qualifiers

1. 139934

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="genomic DNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/chromosome="1"

/clone="P0506E04"

/complement(2636, 2911)

/gene="P0506E04.1"

/complement(2636, 2911)

/codon_start=1

/product="putative anther-specific protein"

/protein_id="BAB67924.1"

/db_xref="GI:15623866"

/translation="MVRVGAANAIVLIALAANAAMAAPEPTDDGAVRVAGLTKCVSGGSKVTSCLIGCYGGGGGAAATAAMPFCVIGCTSVLSCATGCSYSL"

/complement(7104, 7325)

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/complement(7104, 7325)

/gene="P0506E04.2"

/note="hypothetical protein"

/codon_start=1

/protein_id="BAB67925.1"

/db_xref="GI:15623867"

/translation="MLPLAASGDRVVAAPASTGAGCGEADQCVSRCTVGMQACEAEASRCARATSRRGCGCGCCENEYICGTDIC"

/complement(8282, 8571, 8987, 9075, 10074, 10218, 11724, 11916, 13135, 13286, 13715, 13963, 14517, 14647, 15760, 15818)

/gene="P0506E04.3"

/complement(8282, 8571, 8987, 9075, 10074, 10218, 11724, 11916, 13135, 13286, 13715, 13963, 14517, 14647, 15760, 15818)

/gene="P0506E04.3"

/note="hypothetical protein"

/codon_start=1

/protein_id="BAB67926.1"

/db_xref="GI:15623868"

/translation="WGAHATLFLVLSLPCSFSSSRPLVAAATTAANAARCCCGGAAALAAARSAGCHQVLVTGCAVSPRRGGVPLPPPPAPPLCCASSSRVARRRPHLLDKHKMSFTFAALPPSQQLCAAGSPNSVALDLDTSPASVLANHMTADSDSPRHMLQGIQCRKSNFSTREPRPPGSPALSPASPSPPRRSVAAAAYGCGDVMRPFDTQITLISAVSVSLVSLGLTKTKGTGMQSPYCNPKRLOEERKRTAAVHQSGSPLISGPAATLTLESGTTPPPNDAAVDAVCAHAGKSEAAAMPPTVTVTYSSPSBSPTHQULPRACRLIRRRHLLSHGCKSAADVAAYVRESDIARAPRIIRLLDBRGSIVIAEELISALAVGGGRSVYCTIREDNYIKLIDHFY"

/complement(11717, 17487, 17699, 18031)

/gene="P0506E04.4"

/complement(11717, 17487, 17699, 18031)

/gene="P0506E04.4"

/note="hypothetical protein"

/codon_start=1

/protein_id="BAB67927.1"

/db_xref="GI:15623869"

REFERENCE	2 (Pages 1 to 118649)
AUTHORS	Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE	Submitted (19-FEB-2001) Takui Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
JOURNAL	E-mail: tsukuba.ibaraki.go.jp, URL: http://rgp.daffrc.go.jp/, Tel: 81-298-38-7441, Fax: 81-298-38-7468
COMMENT	On May 22, 2002 this sequence version replaced g1:15080711. Genes were predicted from the integrated results of the following: GENSCAN1.0, BLAST2.0, BLASTX.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI Nonredundant protein database, nt (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RCP. Protein homologues of the coding regions were searched against NCBI Nonredundant protein database with BLAST2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding RCP accession no. and RCP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, putative- and -like protein. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein. The orientation of the sequence is from 5' to 3' of the PAC clone. This sequence of P0423A12 clone has an overlap with P0506A04 clone (DBD: AP003272) at the position 1 to 56,253 of 5' end and an overlap with P0492G09 clone (DBD: AP003266) at the position 91,496 to 178,649 of 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.daffrc.go.jp/Genomeseq.html.
FEATURES	Location/Qualifiers
SOURCE	1. 178649
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	/submitter="Nipponbare"
	/db_xref="taxon:39947"
	/chromosome="1"
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gene	join(9349..9492,9624..9855,9939..10041,10587..10707,10799..10942,11658..11737,11818..11898,11989..12007)
	/gene="P0423A12.3"
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gene	join(12865..13367,13481..13556,14087..14255,14754..14869,14901..15097,15434..15590)
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gene	join(16686..16720,17573..17698,18010..18341,18350..18396,18401..18709)
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	/note="hypothetical protein"
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gene	join(20205..20630,20205..20630)
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CDS	join(20205..20630)
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	/note="hypothetical protein"
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gene	join(23341..24179,24747..25116,26071..26141,27080..27125,27589..27811,27919..28122)
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	/db_xref="GI:21104647"
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gene	complement(join(34576..34695,34775..34801,35227..35265))

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 23, 2003, 05:57:28 ; Search time 214 Seconds
(Without alignments)
1046.978 Million cell updates/sec

Title: US-09-854-562-2

Sequence score: 445
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Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	434.5	97.6	506	22	AAFB3987	Pepper defensin pr
2	431.5	97.0	548	24	ABX12800	DNA encoding Capsi
3	189.5	42.6	566	20	AAV70142	Nicotiana excelsio
4	182.5	41.0	564	12	AAQ0262	Ovary tissue trans
5	182.5	41.0	564	14	AAQ34940	p2130 coding seque
6	182.5	41.0	564	17	AA731823	Tomato p2130 cDNA
7	182.5	41.0	564	18	AA748813	cDNA clone p2130 c
8	182.5	41.0	564	24	ABZ21970	Plasmid p2130 cDNA
9	177.5	39.9	558	20	AAV70143	Nicotiana panicula
10	156	35.1	456	20	AAV70141	Nicotiana excelsio
11	152	29.7	3528	17	AA731824	Tomato p2130 genom
12	152	29.7	3528	18	AA748816	Calgene Lambda 140
13	152	29.7	3528	24	ABZ21971	Plasmid p2130 cDNA
14	152	29.7	4383	12	AAQ0263	p2130 contig. Calge
15	152	29.7	4383	12	AAQ0319	Calgene lambda 140
16	152	29.7	4383	14	AAQ35143	Calgene lambda 140
17	132	29.7	4383	14	AAQ34941	Calgene lambda 140
18	132	29.7	4383	14	AAQ34941	Calgene lambda 140
19	86.5	19.4	272	25	ABX28732	Human GDP-mannose
20	86.5	19.4	272	25	ABX29735	Human GDP-mannose
21	84.5	19.0	465	21	ABX19080	Human GDP-mannose
22	84.5	19.0	520	21	AAQ35542	Arabidopsis thailia
23	84	18.9	594	17	AA716870	Arabidopsis thailia
24	84	18.9	594	22	AA716870	Pepper Group 2 pro
25	83.5	18.8	275	25	ABX22337	Human GDP-mannose
26	81	18.2	234	24	ABZ12813	Human GDP-mannose
27	81	18.2	425	25	ABX62145	Arabidopsis thailia
28	79	17.8	225	22	AAFB3988	Pepper thionin-lik
29	79	17.8	2000	24	ABZ15483	Arabidopsis thailia
30	77.5	17.4	597	21	AAQ40605	Arabidopsis thailia
31	77	17.3	294	24	ABZ17690	Arabidopsis thailia
32	76.5	17.2	2297	22	AAH79909	Corn tassal-derive
33	74.5	16.7	1216	22	AAZ34468	C albicans apoptos
34	74	16.6	403	19	AAV10632	Mouse-15 kDa selen
35	74	16.6	697	21	AA714323	A. thaliana FDF1.1
36	73.5	16.5	2263	21	AA714323	Aspergillus oryzae
37	73.5	16.5	2410	22	AAQ6109	Human ORF ORF1664
38	73.5	16.5	2569	22	AAQ6109	Human full-length
39	73.5	16.5	3593	22	AAQ6109	Human secreted pro
40	73.5	16.5	5586	22	AAQ6109	Human cDNA encodin
41	73.5	16.5	5586	22	AAQ6109	Tumour suppressor
42	73.5	16.5	5586	22	AAQ6109	Human immune syste
43	73	16.4	282	21	AAQ6109	Drosophila melanog
44	73	16.4	334	21	AAQ6109	Arabidopsis thailia
45	72.5	16.3	264	25	ABX31561	Arabidopsis thailia

ALIGNMENTS

RESULT 1	AAFB3987
ID	AAFB3987 standard; cDNA to mRNA; 506 BP.
AC	AAFB3987;
XX	22-AUG-2001 (first entry)
DT	Pepper defensin protein gene, PeppDef cDNA sequence.
XX	Pepper; defensin; PeppDef; thionin-like protein; PeppThi; transgenic;
KW	phytopathogen; antimicrobial; ss.
XX	Capsicum annuum.
OS	
XX	
FT	Key Location/Qualifiers
CDS	10..264

```

FT  /*tag= a
FT  /product= "defensin protein"
FT  /gene= "Pepef"
XX  EPI101771-A1.
XX  23-MAY-2001.
XX  15-NOV-1999; 99EP-0309059.
XX  15-NOV-1999; 99EP-0309059.
XX  (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX  Oh B, Ko MK, Shin B, Chung CH;
XX  WPI; 2001-357927/38.
XX  P-PSDB; AAB85079.
XX  New pathogen induced genes (pepper defensin protein gene and pepper
XX  thionin-like protein gene) from Capsicum annuum, useful for producing
XX  transgenic plants with enhanced resistance against phytopathogens, e.g.
XX  fungi or nematode.
XX  Claim 3; Page 10-11; 22pp; English.
XX  The invention provides new isolated nucleic acid molecules encoding a
XX  pepper defensin protein (Pepef) and a pepper thionin-like protein
XX  (Peptih). The Pepef and Peptih genes are useful for producing transgenic
XX  plants that exhibit enhanced resistance against phytopathogens, e.g.
XX  fungi, bacteria, viruses, nematode, mycoplasma-like organisms, parasitic
XX  higher plants, flagellate protozoa or insects. The present sequence
XX  represents the cDNA sequence of the Pepef gene.
XX  Sequence 506 BP; 174 A; 74 C; 96 G; 162 T; 0 other;
XX  Alignment Scores:
XX  Pred. No.: 7.43e-45 Length: 506
XX  Score: 434.50 Matches: 83
XX  Percent Similarity: 98.81% Conservative: 0
XX  Best Local Similarity: 98.81% Mismatches: 0
XX  Query Match: 97.64% Indels: 1
XX  DB: 22 Gaps: 1
XX  US-09-854-562-2 (1-83) x AAF83987 (1-506)
XX  QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuAa---ThrluPheValAa 19
XX  Db 10 ATGGCTCGTTCATTTACTTCATGCAATTTCTTGCTTGGCAATGACACCTTTGTTGCT 69
XX  QY 20 TyrgIValGInglYlysgIuileCysCysIysGluLeuThrIysProValIysCysSer 39
XX  Db 70 TATGGGGGTCAAGGCAAGAAATTTGCTGTAAAGCTCCAAAACTGTTAAATGTTCT 129
XX  QY 40 SerAspProLeuCyseGluIysLeuCyseMetGluIysGluIysTyrGluAspGlyHsCys 59
XX  Db 130 AGTGACCCCTTATGTAATAAACTGTATGAGAAAGCAAAATGTGAAGATGCTCATTTGT 189
XX  QY 60 PheThrIleLeuSerIysCyseLeuCyseMetIysAspCysAsnAlaIysThrLeuAlaThr 79
XX  Db 190 TTCACATCTCTAAGCAAGATGCTTATGCAATGAAGATGTATGCTAAAACTCCGGAACA 249
XX  QY 80 GluLeuLeuAla 83
XX  Db 250 GAATTCCTTCT 261
XX  RESULT 2
XX  ID ABL12800 standard; DNA; 548 BP.
XX  AC ABL12800;
XX  DT 29-MAY-2003 (first entry)

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XX  DNA encoding Capsicum annuum L. cv. Hanbyul thionine.
XX  Thionine; plant disease resistance; plant; gene; ds.
XX  Capsicum annuum L. cv. Hanbyul.
XX  Key Location/Qualifiers
XX  CDS 52..306
XX  /*tag= a
XX  /product= "Thionine"
XX  /transl_except= (pos:64..66,aa:Thr)
XX  /transl_except= (pos:271..273,aa:Xaa)
XX  /note= "Xaa is given as "Net" in the specification"
XX  KR2002024732-A.
XX  01-APR-2002.
XX  26-SEP-2000; 2000KR-0056518.
XX  26-SEP-2000; 2000KR-0056518.
XX  (KOCU-) KOREA CHUNGANG EDUCATIONAL FOUND.
XX  Hwang BG, Kim YJ, Lee SC;
XX  WPI; 2002-747901/81.
XX  P-PSDB; AB008325.
XX  Thionine gene of Capsicum annuum L. cv. hanbyul and probing method of
XX  resistance for plant diseases -
XX  Example 1; Fig 1; 14pp; Korean.
XX  The present invention relates to the thionine gene of Capsicum
XX  annuum L. cv. Hanbyul, and a probing method of resistance for
XX  plant diseases caused by Xanthomonas campestris subsp. vesicatoria.
XX  Collectotrichum coccodes, Collectotrichum gloeosporioides and the like.
XX  The presents sequence encodes Capsicum annuum L. cv. Hanbyul thionine.
XX  Sequence 548 BP; 188 A; 76 C; 105 G; 179 T; 0 other;
XX  Alignment Scores:
XX  Pred. No.: 1.95e-44 Length: 548
XX  Score: 431.50 Matches: 82
XX  Percent Similarity: 98.81% Conservative: 1
XX  Best Local Similarity: 97.62% Mismatches: 0
XX  Query Match: 96.97% Indels: 1
XX  DB: 24 Gaps: 1
XX  US-09-854-562-2 (1-83) x ABL12800 (1-548)
XX  QY 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuAa---ThrluPheValAa 19
XX  Db 52 ATGGCTCGTTCATTTACTTCATGCAATTTCTTGCTTGGCAATGACACCTTTGTTGCT 111
XX  QY 20 TyrgIValGInglYlysgIuileCysCysIysGluLeuThrIysProValIysCysSer 39
XX  Db 112 TATGGGGGTCAAGGCAAGAAATTTGCTGTAAAGCTCCAAAACTGTTAAATGTTCT 171
XX  QY 40 SerAspProLeuCyseGluIysLeuCyseMetGluIysGluIysTyrGluAspGlyHsCys 59
XX  Db 172 AGTGACCCCTTATGTAATAAACTGTATGAGAAAGCAAAATGTGAAGATGCTCATTTGT 231
XX  QY 60 PheThrIleLeuSerIysCyseLeuCyseMetIysAspCysAsnAlaIysThrLeuAlaThr 79
XX  Db 232 TTCACATCTCTAAGCAAGATGCTTATGCAATGAAGATGTATGCTAAAACTCCGGAACA 291
XX  QY 80 GluLeuLeuAla 83
XX  Db 292 GAATTCCTTCT 303

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RESULT 3
AAV70142
ID AAV70142 standard; cDNA to mRNA; 566 BP.
XX
AC AAV70142;
XX
DT 03-FEB-1999 (first entry)
XX
DE Nicotiana excelsior thionine gene Neth12.
XX
KW Nicotiana excelsior; Nicotiana paniculata; thionine; Neth11; Neth12;
XX
OS Nicotiana excelsior.
XX
FH Key Location/Qualifiers
FT CDS 33..350
FT /tag= a
XX
PN JP10295380-A.
XX
PD 10-NOV-1998.
XX
PF 23-APR-1997; 97JP-0120179.
XX
PR 23-APR-1997; 97JP-0120179.
XX
PA (NIBS) JAPAN TOBACCO INC.
XX
DR WPI; 1999-038278/04.
XX
DR P-PSDB; AAW63132.
XX
PT Thionine gene derived by salt stress - used to deliver improved salt
PT stress to plants
XX
PS Claim 3; Page 5; 6pp; Japanese.
XX
CC The present sequence represents a thionine gene from Nicotiana excelsior
CC derived Neth12. The thionine protein has an effect of improving the salt
CC stress resistance of a plant. The gene can improve the salt stress
CC resistance of a plant.
XX
SQ Sequence 566 BP; 178 A; 94 C; 108 G; 186 T; 0 other;
XX
Alignment Scores:
Pred. No.: 2,65e-14 Length: 566
Score: 189.50 Matches: 43
Percent Similarity: 60.00% Conservative: 11
Best Local Similarity: 47.78% Mismatches: 25
Query Match: 42.58% Indels: 11
DB: 20 Gaps: 3
XX
US-09-854-562-2 (1-83) x AAV70142 (1-566)
OY 1 MetAlaAGSerIleTyRPhemeAlaPheUeuValIeuAlaThr---LeuPheValAla 19
DB 33 ATGGCTCGCTCGTGGTGGCTTCAATGCAATTTGCTATCTTGGCAGTGATGCTCTTTGTTGCC 92
OY 20 TTYGlyValGlnGlyLVeGlnIleCysCysAluysGluuThrIysProValIysCysSer 39
DB 93 TATGAGTGTGAAGCTAAAGATTGCAAAACAGAAAGCAATTCATCCCTGGAAATATGCATT 152
OY 40 SerAspProLeuCySglnIuysLeuCySmetGluysGlnIuysTYrgIuAepGIyH; sCys 59
DB 153 ACCAAACCAACATGCAAGAAAGCTTGTATC---AAAGAGAAATTTACTGATGCTCATTTGT 209
OY 60 PheThrIleLeuSerIysCySleuCySweIysAlrGys----- 72
DB 210 AGCAAAATCTCTGAGAGGTGTCTATGCACTAAGCATGTGTGTTGATGAGAAATGATC 269
OY 73 -----AsnAlaIysThrIeuAlaThrGlu 80
DB 270 AAAACAGAGAGCTGAACCTTACTGATGAGAA 299

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RESULT 4
AAQ10262
ID AAQ10262 standard; cDNA; 564 BP.
XX
AC AAQ10262;
XX
DT 25-MAR-2003 (updated)
DT 04-APR-1991 (first entry)
XX
DE Ovary tissue transcriptional factor DNA clone pz130.
XX
KW Ovary tissue transcriptional factor; DNA construct; probe;
XX
OS Lycopersicon esculentum UC92B.
XX
FH Key Location/Qualifiers
FT misc_feature 447..564
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FT /label= pz7_probe
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PN EP409629-A.
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PD 23-JAN-1991.
XX
PF 19-JUL-1990; 90EP-0307926.
XX
PR 19-JUL-1989; 89US-0382518.
XX
PA (CALJ) CALGENE INC.
XX
PI Martineau B, Houck CM;
XX
DR WPI; 1991-024191/04.
XX
DR P-PSDB; AAR10310.
XX
PT New ovary tissue transcriptional factors - modify transcription
PT in tomato plant ovaries for use as mol. probes
XX
PS Disclosure; Fig 1; 21pp; English.
XX
CC The tomato-derived transcriptional initiation region which regulates
CC the expression of the sequence corresp. to the pz130 clone is
CC considered ovary-specific. Sequences hybridizable to the pz130
CC clone, e.g. probe pz7, show abundant mRNA, esp. at the early stages
CC of anthesis. The message is expressed in ovary integument and ovary
CC outer pericarp tissue and is not expressed, or at least not readily
CC detectable, in other tissues or at any other stage of fruit
CC development. The native function of the amino acid sequence
CC encoded by the structural gene comprising pz130 is unknown.
CC See also AAQ10263-64.
XX
SQ Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;
XX
Alignment Scores:
Pred. No.: 1.96e-13 Length: 564
Score: 182.50 Matches: 41
Percent Similarity: 62.35% Conservative: 12
Best Local Similarity: 48.24% Mismatches: 29
Query Match: 41.01% Indels: 3
DB: 12 Gaps: 3
XX
US-09-854-562-2 (1-83) x AAQ10262 (1-564)
OY 1 MetAlaAGSerIleTyRPhemeAlaPheUeuValIeuAla---ThrIeuPheValAla 19
DB 40 ATGGCTCGCTCGTGGTGGCTTCAATGCAATTTGCTTGGCAATGATGCTCTTTGTTACC 99
OY 20 TTYGlyValGlnGlyLVeGlnIleCys---CysIysGlnUeuThrIysProValIysCys 38
DB 100 TATGAGTGTGAAGCTCAACAATTTGCAAGCAACCAAGCAAACTTCCAGATATATGT 159

```

Score:	182.50	Matches:	41
Percent Similarity:	62.35%	Conservative:	12
Best Local Similarity:	48.24%	Mismatches:	29
Query Match:	41.01%	Indels:	3
DB:	14	Gaps:	3

US-09-854-562-2 (1-83) x AAQ34940 (1-564)

Qy	1	MetAlaArgSerIleTyrPheMetAlaPheLeuValIleuAla	19
Dd	40	ATGGGTGGTTCATTTTCTTCATGSCATTTTGGTCTGGCAATATGTGTTACC	99
Qy	20	TyrGlyValGlnGlySerGluIleCys---CysArgGluLeuThrIleProValIleCys	38
Dd	100	TATAGAGTAACCTCAGCAAAATTGGCAACACCAACCAACCTTCCAGATTAATGT	159
Qy	39	SerSerAspProLeuGlySerGlnIleLeuGlySerMetGluIleGluSerGluIleAspGlyHis	58
Dd	160	TTTATGGCTTCATCATGATGTAAGAAAATATTGTATC---AAAGAGAAATTTACTGTGGACAT	216
Qy	59	CysPheThrIleLeuSerIleCysIleGlySerMetIleValArgCysAsnAlaIleThrLeuAla	78
Dd	217	TGTAGCAAACTCCAAAGAGAGTCTATGACCTAAGCCATGTATTTGACAAATCTCA	276
Qy	79	ThrGluLeuLeuAla	83
Dd	277	AGTGAAGTTAAAGCA	291

RESULT 6
AATJ1823
ID AATJ1823 standard; cDNA; 564 BP.
AC AATJ1823;
XX 25-MAR-2003 (updated)
DT 14-SEP-1996 (filter entry)
XX Tomato pz130 cDNA clone.
DE Ovary; ovule; fruit; tomato; cotton; melanin; vector;
XX transgenic plant; ss.
XX Lycopodium esculentum cv. UC82B.
XX Key Location/Qualifiers
FT CDS 1..357
FT /*tag= a
XX US5530185-A.
XX 25-JUN-1996.
XX 29-DEC-1992; 92US-0998158.
XX 29-DEC-1992; 92US-0998158.
XX 19-JUL-1989; 89US-0382518.
XX 17-JUL-1990; 90US-0554195.
XX (CALD) CALGENE INC.
XX Martineau BM, Reilley AA, Stalker DM;
PI WPI; 1996-308822/31.
DR P-PSDB; AAR97/559.
XX DNA construct for expressing melanin synthesis gene in plant ovule
PT cells - contains promoter from the tomato pz130 gene, also binary
PT vector and transgenic plants, esp. cotton, confg. construct
XX
XX Example 3; Fig 1A-B; 25pp; English.
XX The tomato pz130 clone contains a 564 bp insert of cDNA (AATJ1823)
XX detected only in a tomato cDNA library prep'd. from pre-anthesis

CC RNA. It was isolated by screening a library prep'd. from cDNA
 CC of pre-anthesis stage ovaries with probes made from pre-anthesis
 CC mRNA, leaf mRNA and young seedling mRNA. The insert was used to
 CC isolate the corresponding genomic clone (AAT4814). The p2130
 CC transcriptional initiation region is considered to be ovary-specific.
 CC It can be utilised in DNA constructs for the expression of
 CC heterologous genes, partic. in early fruit development, and esp. for
 CC expression of a melanin synthesis gene in transgenic cotton. The
 CC native function of the p2130 gene product (AAT4814) is unknown.
 CC (updated on 25-MAR-2003 to correct P field.)
 CC
 XX Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 1,966-13 Length: 564
 Score: 182.50 Matches: 41
 Percent Similarity: 62.35% Conservative: 12
 Best Local Similarity: 48.24% Mismatches: 29
 Query Match: 41.01% Indels: 3
 DB: 17 Gaps: 3
 US-09-854-562-2 (1-83) x AAT4813 (1-564)
 QY 1 MetAlAAAGSerIleTyPheMetAlAPheLeuValIleuA1a 19
 Db 40 ATGGCTCGTTCATTTCTTCATGCGCATTTTGGCTTGCATGATGCTCTTTGTACC 99
 QY 20 TyGlyValGInGlyLysGluIleCys---CysLysGluLeuThrLysProValLysCys 38
 Db 100 TATGAGTGAAGCTCAGCAAAATTGGCAAGCACCAGCAAACTTCCCGAGATTATGT 159
 QY 39 SerSerAspProLeuCysGlnLysLeuCysMetGlnLysGlnLysTyGlnAspGlyHis 58
 Db 160 TTTATGACTCATCATCTGAGAAATATTGTATC---AAAGAGAAATTACTGCTGACAT 216
 QY 59 CysPheThrIleLeuSerLysCysLeuCysMetLysArgCysAsnAlaLysThrLeuA1a 78
 Db 217 TGTAGCAACTCCAAAGAGAGTCTATGCACTAGCCATGTGATTATGGCAAAATCTCA 276
 QY 79 ThrGluLeuLeuA1a 83
 Db 277 AGTGAAGTTAAAGCA 291
 RESULT 7
 AAT4813
 ID AAT4813 standard; cDNA; 564 BP.
 XX
 AC AAT4813;
 XX
 DT 14-MAR-1997 (first entry)
 XX
 DE cDNA clone p2130 capable of directing ovary-tissue transcription.
 XX
 KM Ovary; fruit; colour; pigmentation; cotton; tomato; probe;
 KM promoter; p2130; p27; transgenic plant; ds.
 XX
 OS Lycopersicon esculentum cv. UC82B.
 XX
 FH Key Location/Qualifiers
 FH CDS 1..357
 FT misc_RNA /tag= a
 FT 447..564 /tag= b
 FT /note= "bases 447-564 correspond to clone p27"
 XX
 XX MO9640951-A2.
 XX
 XX 19-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-US09911.
 XX
 XX 07-JUN-1995; 95US-0487087.
 XX

PA (CALT) CALGENE INC.
 PI MCBride K, Stalker DM;
 XX
 DR WPI; 1997-052341/05.
 XX
 DR P-PDSB; AAM08364.
 XX
 PT DNA construct capable of directing ovary-tissue transcription in
 PT plants - useful for modifying colour phenotype, in e.g. cotton
 XX
 PS Example 1; Fig 1; 75pp; English.
 XX
 CC A cDNA clone (AAT4813), designated p2130, comprises a tomato
 CC transcriptional initiation region that is capable of directing
 CC tissue, partic. early in fruit development, e.g. to modify colour
 CC phenotype. It can also be used as a molecular probe. To obtain
 CC p2130, a tomato pre-anthesis stage cDNA library was screened by
 CC differential hybridisation. Clones p27 and p28 that hybridised
 CC only to pre-anthesis probes were used to screen a second cDNA
 CC library, yielding p2130 and p270 (see also AAT4814). A genomic
 CC clone (AAT4816) was also isolated using p2130 as probe.
 XX
 SQ Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;
 Alignment Scores:
 Pred. No.: 1,966-13 Length: 564
 Score: 182.50 Matches: 41
 Percent Similarity: 62.35% Conservative: 12
 Best Local Similarity: 48.24% Mismatches: 29
 Query Match: 41.01% Indels: 3
 DB: 18 Gaps: 3
 US-09-854-562-2 (1-83) x AAT4813 (1-564)
 QY 1 MetAlAAAGSerIleTyPheMetAlAPheLeuValIleuA1a 19
 Db 40 ATGGCTCGTTCATTTCTTCATGCGCATTTTGGCTTGCATGATGCTCTTTGTACC 99
 QY 20 TyGlyValGInGlyLysGluIleCys---CysLysGluLeuThrLysProValLysCys 38
 Db 100 TATGAGTGAAGCTCAGCAAAATTGGCAAGCACCAGCAAACTTCCCGAGATTATGT 159
 QY 39 SerSerAspProLeuCysGlnLysLeuCysMetGlnLysGlnLysTyGlnAspGlyHis 58
 Db 160 TTTATGACTCATCATCTGAGAAATATTGTATC---AAAGAGAAATTACTGCTGACAT 216
 QY 59 CysPheThrIleLeuSerLysCysLeuCysMetLysArgCysAsnAlaLysThrLeuA1a 78
 Db 217 TGTAGCAACTCCAAAGAGAGTCTATGCACTAGCCATGTGATTATGGCAAAATCTCA 276
 QY 79 ThrGluLeuLeuA1a 83
 Db 277 AGTGAAGTTAAAGCA 291
 RESULT 8
 AB221970
 ID AB221970 standard; cDNA; 564 BP.
 XX
 AC AB221970;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE Plasmid p2130 cDNA sequence p27.
 XX
 KM Transcriptional factor; ovary tissue; gene; ss.
 XX
 OS Unspecified.
 XX
 FH Key Location/Qualifiers
 FH CDS 1..564
 FT /tag= a
 FT partial

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FT FT /product= "p2130 protein sequence"
FT FT /trans_except= (pos:355..357,aa:Xaa)
FT FT /trans_except= (pos:358..360,aa:Xaa)
FT FT /trans_except= (pos:376..378,aa:Xaa)
FT FT /trans_except= (pos:385..387,aa:Xaa)
FT FT /trans_except= (pos:436..438,aa:Xaa)
FT FT /trans_except= (pos:454..456,aa:Xaa)
FT FT /trans_except= (pos:478..480,aa:Xaa)
FT FT /trans_except= (pos:490..492,aa:Xaa)
FT FT /trans_except= (pos:541..543,aa:Xaa)
FT FT /note= "all Xaa's are encoded by stop codons"
XX XX
XX PN CNI189856-A.
XX PD 05-AUG-1998.
XX XX
XX PF 07-JUN-1996; 96CW-0195170.
XX XX
XX PR 07-JUN-1995; 95US-0480087.
XX XX
XX PA (CALJ ) CALGENE INC.
XX XX WPI; 2002-733392/80.
XX DR P-PSDB; ABP56255.
XX XX
XX PT Use of transcriptional factors of ovary tissue -
XX PS Example 3; Fig 1A-B; 56pp; Chinese.
XX XX
CC CC The present invention describes the use of transcriptional factors of
CC CC ovary tissue. The present sequence represents a nucleotide sequence
CC CC which is used in an example from the present invention.
XX XX
SQ Sequence 564 BP; 188 A; 80 C; 107 G; 189 T; 0 other;

Alignment Scores:
Pred. No.: 1 96e-13 Length: 564
Score: 182.50 Matches: 41
Percent Similarity: 62.358 Conservative: 12
Best Local Similarity: 48.244 Mismatches: 29
Query Match: 41.014 Indels: 3
DB: 24 Gaps: 3

US-09-854-562-2 (1-83) X ABZ21970 (1-564)
QY 1 MetAlaAgSerIleTyRheMetAlaPheLeuValIleuAa---ThrlaPheValaAa 19
Db 40 ATGGCTGCTTCATTTCTTCAAGCAATTTTGGCTTGGCATATGATGCTTTTGTACC 99
QY 20 TYRGIValGInGlyLysGluIleCys---CysLysGluLeuThrluysProValIlyCys 38
Db 100 TATGAGGTGAGAGCTCAGCAATTTGCAAGCACCAAGCCAAACTTCCAGGATTAATGT 159
QY 39 SerSerAspProLeuCySGlnLysLeuCyMetGluLysGluLysTyRgluAspGlyHis 58
Db 160 TTTATGATCATCATATGTAAGAAATATTGTAATC---AAAGAGAAATTTACTGTGAGACAT 216
QY 59 CysPheThrIleLeuSerIlyCysLeuCySmetIlyAsrGlyAsnAlaIlyThrlaLeuAa 78
Db 217 TGTAGCAAACTCCAAAGAGGTGTATGCACTAAGCAATGTGATTTGACAAATCTCA 276
QY 79 ThrGluLeuLeuAa 83
Db 277 ACTGAAGTTAAAGCA 291

RESULT 9
AAV70143
ID AAV70143 standard; cDNA to mRNA; 558 BP.
XX AC AAV70143;
XX XX
XX DT 03-FEB-1999 (first entry)
XX XX

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DB DB Nicotiana paniculata thionine gene NpTH11.
XX XX
XX KW Nicotiana excelsior; Nicotiana paniculata; thionine; NpTH1; NpTH12;
XX KW NpTH1; salt stress; resistance; ds.
XX XX
XX OS Nicotiana paniculata.
XX XX
XX FH Key Location/Qualifiers
XX FT CDS 48..368
XX FT /*tag= a
XX XX
XX PN JP10295380-A.
XX XX
XX PD 10-NOV-1998.
XX XX
XX PF 23-APR-1997; 97JP-0120179.
XX XX
XX PR 23-APR-1997; 97JP-0120179.
XX XX
XX PA (NIBS ) JAPAN TOBACCO INC.
XX XX WPI; 1999-038278/04.
XX DR P-PSDB; AAW83133.
XX XX
XX PT Thionine gene derived by salt stress - used to deliver improved salt
XX PS stress to plants
XX PS Claim 5; Page 5-6; 6pp; Japanese.
XX XX
CC CC The present sequence represents a thionine gene from Nicotiana
CC CC paniculata derived NpTH1. The thionine protein has an effect of
CC CC improving the salt stress resistance of a plant. The gene can improve
XX XX the salt stress resistance of a plant.
XX XX
SQ Sequence 558 BP; 175 A; 87 C; 112 G; 184 T; 0 other;

Alignment Scores:
Pred. No.: 8 11e-13 Length: 558
Score: 177.50 Matches: 45
Percent Similarity: 53.00% Conservative: 8
Best Local Similarity: 45.00% Mismatches: 28
Query Match: 39.89% Indels: 19
DB: 20 Gaps: 4

US-09-854-562-2 (1-83) X AAV70143 (1-558)
QY 1 MetAlaAgSerIleTyRheMetAlaPheLeuValIleuAa---ThrlaPheValaAa 19
Db 48 ATGGCTGCTTCCTTGTCTTCAATGCAATTTGCAAGTCTTGGCAATGATGCTTTTGTGCC 107
QY 20 TYRGIValGInGlyLysGluIleCysCysLysGluLeu---ThrluysProValIlyCys 38
Db 108 TATGAGGTGAGAGCTCAGAACTTGTGCAAGCAAGAAAGCAATCATCTCCCTGATTAATGC 167
QY 39 SerSerAspProLeuCySGlnLysLeuCyMetGluLysGluLysTyRgluAspGlyHis 58
Db 168 ATTACCAAAACCACTGAGAAAGAGCTTGTCTC---AGTAGAAATTTACTGATGAGAAAA 224
QY 59 CysPheThrIleLeuSerIlyCysLeuCySmetIlyAsrGlyAsnAlaIlyThrlaLeuAa 72
Db 225 TGTAGCAAAATCTCAGAAAGGTGATTTGCTACCAAGCAATGTATTTGATGAGAAAGATG 284
QY 73 -----AsnAlaIlyThrlaLeuAa 82
Db 285 ATCCAAAGAGAGCTGAAAAATTTGGCCGAGAAAGCAAGAAATTTGGCTGACACTTTGCTT 344

RESULT 10
AAV70141
ID AAV70141 standard; cDNA to mRNA; 456 BP.
XX AC AAV70141;
XX XX
XX DT 03-FEB-1999 (first entry)
XX XX

```

Accession	Gene	Location/Qualifiers
NC_010295.3	Nicotiana excelsior thionine gene NETH11.	
NC_010295.3	Nicotiana excelsior; Nicotiana glauca; thionine; NETH11; NETH12;	
NC_010295.3	NETH11; salt stress; resistance; de.	
NC_010295.3	Nicotiana excelsior.	
NC_010295.3	Key	Location/Qualifiers
NC_010295.3	CDS	1..240
NC_010295.3		/*lag= a
NC_010295.3	JPI0295380-A.	
NC_010295.3	10-NOV-1998.	
NC_010295.3	23-APR-1997;	97JP-0120179.
NC_010295.3	23-APR-1997;	97JP-0120179.
NC_010295.3	(NISEB) JAPAN TOBACCO INC.	
NC_010295.3	WPI; 1999-038278/04.	
NC_010295.3	P-PSDB; AAW63131.	
NC_010295.3	Thionine gene derived by salt stress - used to deliver improved salt stress to plants	
NC_010295.3	Claim 1; Page 4; 6pp; Japanese.	
NC_010295.3	The present sequence represents a thionine gene from Nicotiana excelsior derived NETH11. The thionine protein has an effect of improving the salt stress resistance of a plant. The gene can improve the salt stress resistance of a plant.	
NC_010295.3	Sequence 456 BP; 149 A; 73 C; 88 G; 146 T; 0 other;	
NC_010295.3	Alignment Scores:	
NC_010295.3	Pred. No.:	2,956-10
NC_010295.3	Score:	156.00
NC_010295.3	Percent Similarity:	68.18%
NC_010295.3	Best Local Similarity:	51.52%
NC_010295.3	Query Match:	35.06%
NC_010295.3	DB:	20
NC_010295.3	US-09-854-562-2 (1-83) x AAV70141 (1-456)	
NC_010295.3	16 LeuPheValAlaIArgIyValGInGlyIyGInIleCysCysIyGInIleuThIySPro 35	
NC_010295.3	1 CTCTTGTTCCTGATGAGTGTGCAAGCTAGAGAA--TGCGAAGAGAAATTTTCACTGA 57	
NC_010295.3	36 ValIyGysGysGysGysGysGysGysGysGysGysGysGysGysGysGysGysGysGys 55	
NC_010295.3	58 CTA--TGCAATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTCACATTC 111	
NC_010295.3	56 AspGlyIleCysPheThrIleuSerIyCysIyGInIleuSerIyCysIyGInIleuSerIyCys 74	
NC_010295.3	112 GATGTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 171	
NC_010295.3	75 LysThrIleuAlaThrGlu 80	
NC_010295.3	172 GAAACCTTTAGCTGAGCA 189	
NC_010295.3	RESULT 11	
NC_010295.3	AAT31824	
NC_010295.3	AAT31824 standard; cDNA; 3528 BP.	
NC_010295.3	AAT31824;	
NC_010295.3	25-MAR-2003 (updated)	
NC_010295.3	14-SEP-1996 (first entry)	
NC_010295.3	Tomato p2130 genomic clone calgene lambda 140.	

XX	XX	Ovary; ovule; fruit; tomato; cotton; melanin; vector;
KW	KW	transgenic plant; ss.
OS	OS	Lycopersicon esculentum cv. UC82B.
XX	XX	
FH	FH	Key
FT	FT	misc_difference 586
FT	FT	/tag= a
FT	FT	/note= "base n at position 586 is unidentified"
FT	FT	misc_difference 590
FT	FT	/tag= b
FT	FT	/note= "base n at position 590 is not identified"
FT	FT	misc_difference 591
FT	FT	/tag= c
FT	FT	/note= "base n at position 591 is not identified"
FT	FT	misc_difference 663
FT	FT	/tag= d
FT	FT	/note= "base n at position 663 is not identified"
FT	FT	misc_difference 667
FT	FT	/tag= e
FT	FT	/note= "base n at position 667 is not identified"
FT	FT	misc_difference 769
FT	FT	/tag= f
FT	FT	/note= "base n at position 769 is not identified"
FT	FT	misc_difference 2483
FT	FT	/tag= g
FT	FT	/note= "base 2483 is given as s in the specification"
FT	FT	misc_difference 2485
FT	FT	/tag= h
FT	FT	/note= "base 2485 is given as s in the specification"
FT	FT	exon
FT	FT	2567..2701
FT	FT	/tag= i
FT	FT	2702..2921
FT	FT	/tag= j
FT	FT	2922..3528
FT	FT	exon
FT	FT	/tag= k
PN	PN	US530185-A.
PD	PD	25-JUN-1996.
PP	PP	29-DEC-1992; 92US-0998158.
XX	XX	
XX	XX	29-DEC-1992; 92US-0998158.
PR	PR	19-JUL-1989; 89US-0362518.
PR	PR	17-JUL-1990; 90US-0554195.
XX	XX	
PA	PA	(CALJ) CALGENE INC.
PI	PI	Martineau BM, Reilley AA, Stalker DM;
XX	XX	
DR	DR	WPI; 1996-308822/31.
XX	XX	
DR	DR	P-PSDB; AAR97559.
PT	PT	DNA construct for expressing melanin synthesis gene in plant ovule
PT	PT	cells - contains promoter from the tomato pz130 gene, also binary
PT	PT	vector and transgenic plants, esp. cotton, cong. construct
XX	XX	
PS	PS	Example 5; Fig 2A-C; 25pp; English.
XX	XX	
CC	CC	The tomato pz130 genomic clone (AATJ1824) was isolated from a genomic
CC	CC	library using a pz130 cDNA clone (AATJ1823) as probe. The pz130
CC	CC	transcriptional initiation region is considered to be ovary-specific.
CC	CC	It can be utilized in DNA constructs for the expression of
CC	CC	heterologous genes, partic. in early fruit development, and esp. for
CC	CC	expression of a melanin synthesis gene in transgenic cotton. The
CC	CC	native function of the pz130 gene product (AAR97559) is unknown.
CC	CC	(Updated on 25-MAR-2003 to correct PF field.)
XX	XX	
SQ	Sequence	3528 BP; 1191 A; 529 C; 518 G; 1282 T; 8 other;

Alignment Scores:

Pred. No.:	4,21e-06	Length:	3528
Score:	132.00	Matches:	42
Percent Similarity:	33.33%	Conservative:	11
Best Local Similarity:	26.42%	Mismatches:	29
Query Match:	29.66%	Indels:	77
DB:	17	Gaps:	4

US-09-854-562-2 (1-83) x AAT31824 (1-3528)

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QY      1 MetAlaAgSerIleTyRPhMeAlaPheLeuValLeuA1a---ThirLeuPheVala1a 19
D      2638 ATGGCTGCTTCATTTCTTCATGCGATTTTGGCTTGGCAATGATGCTCTTGTACC 2697
QY      20 TYGlyValGlnGly-----
D      2698 TATGGTTTGCTTCATTAATTTATTCCTCAAAATCATCGCAATAAAAAATGTAACG 2757
QY      25 lvsGluIleCysCyslvsGluLeuThrIys-ProValIys-----
D      2758 AAGCAGACATCAGTAACCGTTTAATAATACCCTTAATAAATTTGTAATGATATTACTT 2817
QY      37 -----
D      2818 GCTATACGTTTAACAATGATGATAAAAAAACCTAAATATATTACTTATTGATTTGCTCT 2877
QY      37 -----
D      2878 CTCTCATGTTATTCTAATTTTGTGTGTAATGATGTAGAGTAGAAGCTCAGCA 2937
QY      38 -----
D      2938 AATTTCAAAGCACCAGCCAACTTCCAGATTAATGTTTATGACATCATCATGATG 2997
QY      45 nlylsleuCySmelIySArgCysAsnAlaIySThirLeuAlaThrGluLeuLeuA1a 65
D      2998 AAAATATTGTATC---AAAGAGAAATTTACTGTGGACATTTGTAGCAAACTCCAAAGCA 3054
QY      65 sCysleuCySmelIySArgCysAsnAlaIySThirLeuAlaThrGluLeuLeuA1a 83
D      3055 GTGCTATGACACTAAGCCATGTGTATTGACAAATCTCAAGTGAAGTTAAAGCA 3109

RESULT 12
ID      AAT48816 standard; cDNA, 3528 BP.
XX      AAT48816;
AC      AAT48816;
XX      14-MAR-1997 (first entry)
DT      14-MAR-1997 (first entry)
XX      Calgene Lambda 140 genomic clone.
DE      Ovary; fruit; colour; pigmentation; cotton; tomato; probe;
KM      promoter; p2130; p27; transgenic plant; ss.
XX      Lycopersicon esculentum cv. UC82B.
OS      Lycopersicon esculentum cv. UC82B.
XX      Key
FH      Location/Qualifiers
FT      exon
FT      2567..2701
FT      /tag= a
FT      intron
FT      2702..2921
FT      /tag= b
FT      exon
FT      2922..3528
FT      /tag= c
FT      misc_RNA
FT      2599..2701
FT      /tag= d
FT      /note= "5' end of p2130 gene"
FT      2922..3382
FT      /tag= e
FT      /note= "3' end of p2130 gene"
XX      PN      WO9640951-A2.

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XX      PD      19-DEC-1996.
XX      PF      07-JUN-1996; 96WO-US09911.
XX      PR      07-JUN-1995; 95US-0487087.
XX      PA      (CALJ ) CALGENE INC.
XX      PI      McBride K, 'Salk' DM;
XX      DR      WPI; 1997-052341/05.
XX      PT      DNA construct capable of directing ovary-tissue transcription in
XX      plants - useful for modifying colour phenotype, in e.g. cotton
XX      PS      Example 7; Fig 2; 75pp; English.
XX      CC      Calgene Lambda 140 genomic clone (AAT48816) overlaps with the
XX      CC      tomato ovary-specific p2130 cDNA clone (see also AAT48813) and
XX      CC      includes regions 5' and 3' to p2130. It was isolated from a
XX      CC      tomato cv. UC82B genomic library using p2130 as probe. The
XX      CC      genomic clone can be used to construct p2130 promoter cassettes
XX      CC      useful for directing ovary tissue transcription in plants, e.g. to
XX      CC      modify colour phenotype in cotton.
XX      SQ      Sequence 3528 BP; 1191 A; 529 C; 518 G; 1282 T; 8 other;

Alignment Scores:
Pred. No.: 4,21e-06 Length: 3528
Score: 132.00 Matches: 42
Percent Similarity: 33.33% Conservative: 11
Best Local Similarity: 26.42% Mismatches: 29
Query Match: 29.66% Indels: 77
DB: 18 Gaps: 4

US-09-854-562-2 (1-83) x AAT48816 (1-3528)
QY      1 MetAlaAgSerIleTyRPhMeAlaPheLeuValLeuA1a---ThirLeuPheVala1a 19
D      2638 ATGGCTGCTTCATTTCTTCATGCGATTTTGGCTTGGCAATGATGCTCTTGTACC 2697
QY      20 TYGlyValGlnGly-----
D      2698 TATGGTTTGCTTCATTAATTTATTCCTCAAAATCATCGCAATAAAAAATGTAACG 2757
QY      25 lvsGluIleCysCyslvsGluLeuThrIys-ProValIys-----
D      2758 AAGCAGACATCAGTAACCGTTTAATAATACCCTTAATAAATTTGTAATGATATTACTT 2817
QY      37 -----
D      2818 GCTATACGTTTAACAATGATGATAAAAAAACCTAAATATATTACTTATTGATTTGCTCT 2877
QY      37 -----
D      2878 CTCTCATGTTATTCTAATTTTGTGTGTAATGATGTAGAGTAGAAGCTCAGCA 2937
QY      38 -----
D      2938 AATTTCAAAGCACCAGCCAACTTCCAGATTAATGTTTATGACATCATCATGATG 2997
QY      45 nlylsleuCySmelIySArgCysAsnAlaIySThirLeuAlaThrGluLeuLeuA1a 65
D      2998 AAAATATTGTATC---AAAGAGAAATTTACTGTGGACATTTGTAGCAAACTCCAAAGCA 3054
QY      65 sCysleuCySmelIySArgCysAsnAlaIySThirLeuAlaThrGluLeuLeuA1a 83
D      3055 GTGCTATGACACTAAGCCATGTGTATTGACAAATCTCAAGTGAAGTTAAAGCA 3109

RESULT 13
ID      AB221971 standard; cDNA, 3528 BP.

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```

Db 2638 ATGGCTGCTTCATTTCTTCATGCGATTTTGGCTTGGCAAGAGCGCTTGTGTACC 2697
Qy 20 TYRGLYVALGIngly----- 24
Db 2698 TAAAGTTTGTCTTCATTAATTTATCTCTAAATCATCGCAATAAAAAATGTAAAG 2757
Qy 25 LysGluIleCyScyLysGluLeuThrLys-ProValLys----- 37
Db 2758 AAGCAGACATCATGTAACCGTTTAATTAACCGTTAAAAAATGTGAATGATTTACTT 2817
Qy 37 ----- 37
Db 2818 GCTATACGTTTAAACAATATGATAAAAAACCTTAATAATTAATTTGATTCGCTCT 2877
Qy 37 ----- 37
Db 2878 CTCTCATGTTATCTACTATTTTGTGTGTGAATGATTTAGAGTAGAAGCTCAGCA 2937
Qy 38 -----CysSerSerAspProLeuCyseI 45
Db 2938 AATTTCGAAAGCAGCAAGCAAACTTCCAGAGATTATGTTTATGAGACTCATCATGTAG 2997
Qy 45 nlyslLeuCyseMetGluLysGluLysTYRGLYAspGlyHISCysePheThrIleLeuSerly 65
Db 2998 AAAATATTGTATC---AAAGAGAAATTACTGTGGACATGTGTGCAAACTCCAAAGGAA 3054
Qy 65 sCyseLeuCyseMetLysArgCyseAsnAlaLysThrLeuAlaThrGluLeuLeuAla 83
Db 3055 GTGTCTATGACATCAAGCCATGTGTATTGACAAAATCTCAAGTAGAATTAAAGCA 3109

RESULT 15
AAQ10319 standard; cDNA; 4383 BP.
AC AAQ10319;
XX
XX 25-MAR-2003 (updated)
DT 04-APR-1991 (first entry)
XX
XX Calgene lambda 140 genomic clone.
DE
XX p2130; cytokinin; ds.
KM
XX
XX Synthetic.
OS
XX Key location/Qualifiers
FH misc_RNA 2567..3362
FT /tag= a
FT /note= "Sequence homologous to p2130 transcript"
FT misc_RNA 2599..3382
FT /tag= b
FT /note= "Sequence homologous to p2130 CDS"
FT misc_RNA 2702..2921
FT /tag= C
FT /note= "Sequence homologous to p2130 intron"
XX
XX EP409628-A.
XX
XX 23-JAN-1991.
XX
XX 19-JUL-1990; 90EP-0307925.
XX
XX 19-JUL-1989; 89US-0382802.
XX
XX (CALJ ) CALGENE INC.
XX
XX Houck CM, Pear JR, Martineau B, Hiatt W,
XX
XX WPI; 1991-024190/04.
XX
XX Modulating endogenous cytokinin levels - regulatory regions are
XX transformed into plant cells e.g. fruit to modify pheno-type
XX

```

```

XX
XX Disclosure; Fig 3; 39pp; English.
PS
XX
XX The sequence encodes an enzyme in the cytokinin biosynthetic pathway,
CC derived from Z130, and useful in modulating a transformed plant's
CC phenotype eg. fruit maturation, ripening etc.
CC (updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 4383 BP; 1539 A; 620 C; 610 G; 1606 T; 8 other;
SQ

Alignment Scores:
Score: 5.59e-06 Length: 4383
Percent Similarity: 33.33% Matches: 42
Best Local Similarity: 26.42% Conservative: 11
Query Match: 29.66% Mismatches: 29
DB: 12 Gaps: 77
4

US-09-854-562-2 (1-83) x AAQ10319 (1-4383)

Qy 1 MetAlaArgSerIleTyrPheMetAlaPheLeuValLeuAla---ThrLeuPheValAla 19
Db 2638 ATGGCTGCTTCATTTCTTCATGCGATTTTGGCTTGGCAAGAGCGCTTGTGTACC 2697
Qy 20 TYRGLYVALGIngly----- 24
Db 2698 TAAAGTTTGTCTTCATTAATTTATCTCTAAATCATCGCAATAAAAAATGTAAAG 2757
Qy 25 LysGluIleCyScyLysGluLeuThrLys-ProValLys----- 37
Db 2758 AAGCAGACATCATGTAACCGTTTAATTAACCGTTAAAAAATGTGAATGATTTACTT 2817
Qy 37 ----- 37
Db 2818 GCTATACGTTTAAACAATATGATAAAAAACCTTAATAATTAATTTGATTCGCTCT 2877
Qy 37 ----- 37
Db 2878 CTCTCATGTTATCTACTATTTTGTGTGTGAATGATTTAGAGTAGAAGCTCAGCA 2937
Qy 38 -----CysSerSerAspProLeuCyseI 45
Db 2938 AATTTCGAAAGCAGCAAGCAAACTTCCAGAGATTATGTTTATGAGACTCATCATGTAG 2997
Qy 45 nlyslLeuCyseMetGluLysGluLysTYRGLYAspGlyHISCysePheThrIleLeuSerly 65
Db 2998 AAAATATTGTATC---AAAGAGAAATTACTGTGGACATGTGTGCAAACTCCAAAGGAA 3054
Qy 65 sCyseLeuCyseMetLysArgCyseAsnAlaLysThrLeuAlaThrGluLeuLeuAla 83
Db 3055 GTGTCTATGACATCAAGCCATGTGTATTGACAAAATCTCAAGTAGAATTAAAGCA 3109

Search completed: August 23, 2003, 07:11:42
Job time : 218 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 23, 2003, 07:04:48 ; Search time 55 Seconds

(without alignments)
666,087 Million cell updates/sec

Title: US-09-854-562-2

Sequence: 1 MARSIFYFAFLVATLFPVAV.....SKLCKKRCNATLTATELLA 83

Scoring table:

XGAPop 10.0 , XGAPext 0.5
YGAPop 10.0 , YGAPext 0.5
FGAPop 6.0 , FGAPext 7.0
DELop 6.0 , DELext 7.0

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bl0sum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Issued Patents NA:*
2: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfillseq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	434.5	97.6	506	4 US-09-442-631-1 Sequence 1, Appli
2	182.5	41.0	564	3 US-08-984-330-1 Sequence 1, Appli
3	182.5	41.0	564	3 US-08-487-087A-1 Sequence 1, Appli
4	182.5	41.0	564	4 US-08-397-653B-1 Sequence 1, Appli
5	182.5	41.0	564	6 5175095-1 Patent No. 5175095
6	132	29.7	3528	3 US-08-984-320-2 Sequence 2, Appli
7	132	29.7	3528	3 US-08-487-087A-2 Sequence 2, Appli
8	132	29.7	4383	6 US-08-397-653B-2 Patent No. 5175095
9	132	29.7	4383	6 5175095-4 Patent No. 5175095
10	132	29.7	4383	6 517307-1 Patent No. 517307
11	84	18.9	594	1 US-08-289-458-1 Sequence 1, Appli
12	84	18.9	594	2 US-08-761-549-1 Sequence 1, Appli

13	84	18.9	594	3 US-09-127-646-1 Sequence 1, Appli
14	79	17.8	225	4 US-09-442-631-3 Sequence 3, Appli
15	70.5	15.8	6049	5 US-08-793-273C-3 Sequence 3, Appli
16	70.5	15.8	6049	5 PCT-US95-11684-3 Sequence 3, Appli
17	70	15.7	349	1 US-08-543-238-3 Sequence 3, Appli
18	70	15.7	349	1 US-08-420-526-3 Sequence 3, Appli
19	70	15.7	363	1 US-08-543-238-6 Sequence 6, Appli
20	70	15.7	363	1 US-08-420-526-6 Sequence 6, Appli
21	70	15.7	437	1 US-08-543-238-1 Sequence 1, Appli
22	70	15.7	437	1 US-08-420-526-1 Sequence 1, Appli
23	70	15.7	492	1 US-08-543-238-4 Sequence 4, Appli
24	70	15.7	492	1 US-08-420-526-4 Sequence 4, Appli
25	69	15.5	285	1 US-08-627-706-17 Sequence 17, Appli
26	69	15.5	285	3 US-09-103-489-17 Sequence 17, Appli
27	69	15.5	288	1 US-08-377-687-58 Sequence 58, Appli
28	69	15.5	288	1 US-08-777-192-58 Sequence 58, Appli
29	69	15.5	288	3 US-08-971-982-58 Sequence 58, Appli
30	68	15.3	285	1 US-08-627-706-16 Sequence 16, Appli
31	68	15.3	285	3 US-09-103-489-16 Sequence 16, Appli
32	68	15.3	414	1 US-08-377-687-48 Sequence 48, Appli
33	68	15.3	414	1 US-08-777-192-48 Sequence 48, Appli
34	68	15.3	414	4 US-08-971-982-48 Sequence 48, Appli
35	68	15.3	414	4 US-09-077-951-19 Sequence 19, Appli
36	68	15.3	4724	1 US-08-404-665-3 Sequence 3, Appli
37	68	15.3	4724	1 US-08-404-671-3 Sequence 3, Appli
38	68	15.3	4724	1 US-08-404-781-3 Sequence 3, Appli
39	68	15.3	1230025	4 US-09-198-452A-1 Sequence 1, Appli
40	67.5	15.2	490	4 US-09-003-198A-19 Sequence 19, Appli
41	67.5	15.2	507	3 US-08-766-355-10 Sequence 10, Appli
42	67.5	15.2	507	3 US-09-003-198A-10 Sequence 10, Appli
43	67.5	15.2	507	4 US-09-428-805-10 Sequence 10, Appli
44	67.5	15.2	1237	2 US-08-808-793-25 Sequence 26, Appli
45	67.5	15.2	9551	1 US-08-056-200-93 Sequence 93, Appli

ALIGNMENTS

RESULT 1			
US-09-442-631-1			
Sequence 1, Application US/09442631			
Patent No. 6300469			
GENERAL INFORMATION:			
APPLICANT: OH, BOUNG-JUN			
APPLICANT: KO, MOON KYUNG			
APPLICANT: SHIN, BYONGCHUL			
APPLICANT: CHUNG, CHANG HO			
TITLE OF INVENTION: SMALL AND CYSTEINE RICH ANTIFUNGAL DEFENSIN AND			
TITLE OF INVENTION: THIONIN-LIKE PROTEIN GENES HIGHLY EXPRESSED IN THE			
TITLE OF INVENTION: INCOMPATIBLE INTERACTION			
FILE REFERENCE: 1942/44			
CURRENT APPLICATION NUMBER: US/09/442,631			
NUMBER OF SEQ ID NOS: 4			
SOFTWARE: Patentin Ver. 2.0			
SEQ ID NO 1			
LENGTH: 506			
TYPE: DNA			
ORGANISM: Capsicum annuum			
US-09-442-631-1			
Alignment Scores:			
Pred. No.:	1,01e-50	Length:	506
Score:	434.50	Matches:	83
Percent Similarity:	98.81%	Conservative:	0
Best Local Similarity:	98.81%	Mismatches:	0
Query Match:	97.64%	Indels:	1
DB:	4	Gaps:	1
US-09-854-562-2 (1-83) x US-09-442-631-1 (1-506)			
Oy	1 MetAlaArgSerIleTyrPheMetAlaPheValIleuAla---ThirPheValAla 19		
Db	10 AAGCGCTTCATTCATTACTTCATGCAGCTTCTCTTGCATGCAGACCTTTGTGT 69		

QY	20	TYRIGVAVLGIAGNLYLVSGFGLIUECYSCYSLVSGIUEUTHRIYSPROVALYSCYSSER	39
Db	70	TTATGGGATGCAAGCCAGCAAGAAATTTCCTGTAAAGACTCACAAAACCTGTAAATGTTCT	129
QY	40	SEIAPPPTOLEUCYSGINLYSLVLEUCYSWETGULYSGIULYSGTYIGLAPGLYHSCYSS	59
Db	130	ACTGACCCCTCATATCTCAAAATACTGTATGAGGAAGGAAATATGAAATGTCATTGT	189
QY	60	PHETRIILEUSESLVSCYSLVSCYSMELYSATGYSASNAIALYSHRLEUALATHR	79
Db	190	TTCCAAATTCCTTAACCAAGTGTCTTATGCATGAAGAAGATGTATCTAAACTCTCCCAACA	249
QY	80	GIULEULEUALA	83
Db	250	GAATGCTTGCT	261
RESULT 2			
US-08-984-320-1			
Sequence 1, Application US/08984320			
Patent No. 6222097			
GENERAL INFORMATION:			
APPLICANT: McBRIDE, Kevin E.			
APPLICANT: SCALKER, David M.			
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors			
NUMBER OF SEQUENCES: 6			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Calgene, Inc.			
STREET: 1920 Fifth Street			
CITY: Davis			
STATE: CA			
COUNTRY: USA			
ZIP: 95616			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB			
COMPUTER: Apple Macintosh			
OPERATING SYSTEM: Macintosh 7.1			
SOFTWARE: Microsoft Word 5.1 (a)			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/984,320			
FILING DATE:			
CLASSIFICATION:			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US/08/487,087			
FILING DATE: 07-JUN-95			
APPLICATION NUMBER: US/07/998,158			
FILING DATE: 29-DEC-92			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US/07/554,195			
FILING DATE: 17-JUL-90			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US/07/382,518			
FILING DATE: 19-JUL-89			
ATTORNEY/AGENT INFORMATION:			
NAME: Donna E. Scherer			
REGISTRATION NUMBER: 34,719			
NAME: Carl J. Schwedler			
REGISTRATION NUMBER: 36,924			
REFERENCE/DOCKET NUMBER: CGNE 91-1			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (916) 753-6313			
TELEFAX: (916) 753-1510			
INFORMATION FOR SEQ ID NO: 1:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 564 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: double			
TOPOLOGY: linear			
MOLECULE TYPE: cDNA to mRNA			
US-08-984-320-1			

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Score: 182.50 Matches: 41
Percent Similarity: 62.35% Conservative: 12
Best Local Similarity: 48.24% Mismatches: 29
Query Match: 41.01% Indels: 3
DB: 3 Gaps: 3

US-09-854-562-2 (1-83) x US-08-984-320-1 (1-564)

QY 1 MetaAaArgSerIleTyPheMetAlaPheLeuValLeuAla---ThrluPheValAla 19
Db 40 ATGGCGTGTTCATTTCTTCAAGGCATTGTTGGTCTTGSCAAATGATGCTCTTGGTACC 99
QY 20 TyrclyValInglyLysGluLecys---CylsGluLeuThrLysProValLysCys 38
Db 100 TATAGGATGAACACTCAGCAAAATTGGCAAACCAACCAACCAACCTTCCCGAGATTATGT 159
QY 39 SerSerAspProLeuCysGlnLysLeuCysewctGluLysGluLysTygLuaspGlyHis 58
Db 160 TTATAGCATTCATCATCATGTAGAAAATAATGTATC---AAGAAGAAATTATCGTGACAT 216
QY 59 CysPheThrIleLeuSerLysCysLeuCysewctLysArgCysAsnAlaLysThrLeuAla 78
Db 217 TGTAACAACCTCAAGAAAGTGTATGACCTAACCATGTGTATTGGACAATAATCTCA 276
QY 79 ThrGluLeuLeuAla 83
Db 277 AGTAGAGTTAAAGCA 291

RESULT 3
US-08-487-087A-1
Sequence 1, Application US/08487087A
Patent No. 6268546
GENERAL INFORMATION:
APPLICANT: McBridge, Kevin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087A
FILING DATE: 07-JUN-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

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LENGTH: 564 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-487-087A-1

Alignment Scores:

Score:	4.04e-16	Length:	564
Pred. No.:	182.50	Matches:	41
Percent Similarity:	62.35%	Conservative:	12
Best Local Similarity:	48.24%	Mismatches:	29
Query Match:	41.01%	Indels:	3
DB:	3	Gaps:	3

US-09-854-562-2 (1-83) x US-08-487-087A-1 (1-564)

OY 1 MetAlaArgSerIleTyPheMeAlaPheLeuValIleuA1a---ThrlleuPheValA1a 19
 DB 40 ATGGCTCGTTCATTTCTTCATGGCATTTTGGCTTGGCAATGATGCTCTTGTACC 99
 OY 20 TYRGlyValGlnGlyLysGlnIleCys---CysLysGlnLeuThrlLysProValLysCys 38
 DB 100 TATGAGGTGAAGCTCAGCAAAATTGGCAAGACCAACCAACTTTCCAGGATTATGT 159
 OY 39 SerSerAspProLeuCySGlnLysLeuCySGlnLysGlnLysGlnLysGlnLysGlnLys 58
 DB 160 TTATAGCATCATCATCTGTAAGAAATATTGTATC---AAAGAAATTTACTGTGACAT 216
 OY 59 CysPheThrlleuSerLysCysLeuCySGlnLysGlnLysGlnLysGlnLysGlnLys 78
 DB 217 TGTAGCAAACTCCAAAGAGAGTGTATGACCTAAGCATGTGATTGACAAATCTCA 276
 OY 79 ThrGlnLeuLeuA1a 83
 DB 277 ACTGAAGTTAAAGCA 291

RESULT 4

US-08-397-653B-1

Sequence 1, Application US/08397653B
 Patent No. 6329570

GENERAL INFORMATION:

APPLICANT: Martineau, Belinda
 TITLE OF INVENTION: COTTON MODIFICATION USING
 TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL
 TITLE OF INVENTION: FACTORS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calgene, Inc.
 STREET: 1920 Fifth Street
 CITY: Davis
 STATE: CA
 COUNTRY: USA

ZIP: 95616

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 OPERATING SYSTEM: Macintosh 7.0
 SOFTWARE: Microsoft Word 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/397,653B
 FILING DATE: 28-FEB-1995
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Elizabeth Lassen
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 NAME: Carl J. Schwedler
 REGISTRATION NUMBER: 36,924
 REFERENCE/DOCKET NUMBER: CGNE 112
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313

TELEPAX: (916) 753-1510
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 564 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-397-653B-1

Alignment Scores:

Score:	4.04e-16	Length:	564
Pred. No.: <td>182.50</td> <td>Matches:</td> <td>41</td>	182.50	Matches:	41
Percent Similarity: <td>62.35%</td> <td>Conservative:</td> <td>12</td>	62.35%	Conservative:	12
Best Local Similarity: <td>48.24%</td> <td>Mismatches:</td> <td>29</td>	48.24%	Mismatches:	29
Query Match: <td>41.01%</td> <td>Indels:</td> <td>3</td>	41.01%	Indels:	3
DB: <td>4</td> <td>Gaps:</td> <td>3</td>	4	Gaps:	3

US-09-854-562-2 (1-83) x US-08-397-653B-1 (1-564)

OY 1 MetAlaArgSerIleTyPheMeAlaPheLeuValIleuA1a---ThrlleuPheValA1a 19
 DB 40 ATGGCTCGTTCATTTCTTCATGGCATTTTGGCTTGGCAATGATGCTCTTGTACC 99
 OY 20 TYRGlyValGlnGlyLysGlnIleCys---CysLysGlnLeuThrlLysProValLysCys 38
 DB 100 TATGAGGTGAAGCTCAGCAAAATTGGCAAGACCAACCAACTTTCCAGGATTATGT 159
 OY 39 SerSerAspProLeuCySGlnLysLeuCySGlnLysGlnLysGlnLysGlnLysGlnLys 58
 DB 160 TTATAGCATCATCATCTGTAAGAAATATTGTATC---AAAGAAATTTACTGTGACAT 216
 OY 59 CysPheThrlleuSerLysCysLeuCySGlnLysGlnLysGlnLysGlnLysGlnLys 78
 DB 217 TGTAGCAAACTCCAAAGAGAGTGTATGACCTAAGCATGTGATTGACAAATCTCA 276
 OY 79 ThrGlnLeuLeuA1a 83
 DB 277 ACTGAAGTTAAAGCA 291

RESULT 5

5175095-1

Patent No. 5175095
 APPLICANT: Martineau, Belinda M., Houck, Catherine M.
 TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS
 NUMBER OF SEQUENCES: 9
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/554,195
 FILING DATE: 17-JUL-1990
 SEQ ID NO: 1:
 LENGTH: 564

5175095-1

Alignment Scores:

Score:	4.04e-16	Length:	564
Pred. No.: <td>182.50</td> <td>Matches:</td> <td>41</td>	182.50	Matches:	41
Percent Similarity: <td>62.35%</td> <td>Conservative:</td> <td>12</td>	62.35%	Conservative:	12
Best Local Similarity: <td>48.24%</td> <td>Mismatches:</td> <td>29</td>	48.24%	Mismatches:	29
Query Match: <td>41.01%</td> <td>Indels:</td> <td>3</td>	41.01%	Indels:	3
DB: <td>6</td> <td>Gaps:</td> <td>3</td>	6	Gaps:	3

US-09-854-562-2 (1-83) x 5175095-1 (1-564)

OY 1 MetAlaArgSerIleTyPheMeAlaPheLeuValIleuA1a---ThrlleuPheValA1a 19
 DB 40 ATGGCTCGTTCATTTCTTCATGGCATTTTGGCTTGGCAATGATGCTCTTGTACC 99
 OY 20 TYRGlyValGlnGlyLysGlnIleCys---CysLysGlnLeuThrlLysProValLysCys 38
 DB 100 TATGAGGTGAAGCTCAGCAAAATTGGCAAGACCAACCAACTTTCCAGGATTATGT 159
 OY 39 SerSerAspProLeuCySGlnLysLeuCySGlnLysGlnLysGlnLysGlnLysGlnLys 58

```

Db      160  TTTATGACATCATCATGTACGAAATATTTGATC---AAAGAAATTTACTGCTGCACAT 216
Oy      59  CyshethrllleuseilvscylauCyemclvbaGcYbaSnaillvThrlenua 78
Db      217  TGTGCAAACTCCAAAGGAAAGTGTCTATGACTACCACTGTGTATTGCAAAAATCTCA 278
Oy      79  ThrGluLeuLaua 83
Db      277  AGTGAAGTTAAAGCA 291

RESULT 6
US-08-984-320-2
Sequence 2, Application US/08984320
Patent No. 6222097
GENERAL INFORMATION:
APPLICANT: McBride, Kevin E.
APPLICANT: Stalker, David M.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,320
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087
FILING DATE: 07-JUN-95
APPLICATION NUMBER: US/07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/554,195
FILING DATE: 17-JUL-90
APPLICATION DATA:
APPLICATION NUMBER: US/07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 basepairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-984-320-2

Alignment Scores:
Pred. No.: 4,22e-08 3528
Score: 132.00 42
Percent Similarity: 33.33% Matches:
Best local Similarity: 26.42% Conservative: 11
Query Match: 29.66% Mismatches: 29
DB: 3 Gaps: 4
US-08-984-562-2 (1-83) x US-08-984-320-2 (1-3528)

```

```

0Y      MetAlaAaGSeRiLeTyPhMeEtAlaPhLeuValIleuAla---ThriLeuPheValAla 19
Db      2638 ATGGCTCGTTCATTTTCTTCATGGCATTTTTGCTCTGGCAATGATGCTCTTTGTTCAC 2639
0Y      20  TTTGTLyAlGlnGly----- 24
Db      2698 TATGGTTGTCTTCCTAATATTATTTCCTTAATAATCATCGCAATAAAAAATGTAAGC 2757
0Y      25  LysGluIleCyS/ySgIuLeuThLyS-ProValIys----- 37
Db      2758 AAGCAGACATCAGTAACCGTTTAATAAACCCCTAAAAAAAATTGGAATTGATATTACTT 2817
0Y      37  ----- 37
Db      2818 GCTATTACGTTTAACACTATGATATAAAAAAACCCTAAATAATACTTATTTCGATTTCGCT 2877
0Y      37  ----- 37
Db      2878 CTCCTCATGTTATTCTAACTATTTTGTGTGTGATGATGTAGAGCTGAAGCTCAGCA 2937
0Y      38  -----CysSeSeAspProLeuCySgI 45
Db      2938 AATTTCGAAGACCAACCAACCACTTTCCAGAGATTATGTTTATGACTCATCATGTAG 2997
0Y      45  nLySeuCySMeCtGluLySgIuLyTyrgIuAepGlyhIyS/ySPhethIleLeuSerLy 65
Db      2998 AAAATATTGTATTC---AAAGAGAATTTTACTGTGTGCACATTTGTAGCAAACTCCAAAGCA 3054
0Y      65  gCySLeuCySMeCtLySArgCySAsnAlaLySThrLeuAlaThnGluLeuLeuAla 83
Db      3055 GTCTCATGCACTAAGCCATGTGTATTTCAGCAAAATCTCAAGTGAAGTTAAAGCA 3109

RESULT 7
US-08-487-087A-2
; Sequence 2, Application US/08487087A
; Patent No. 6268546
; GENERAL INFORMATION:
; APPLICANT: McBride, Kevin E.
; APPLICANT: Stalker, David M.
; TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,087A
; FILING DATE: 07-JUN-95
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 07/998,158
; FILING DATE: 29-DEC-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 07/554,195
; FILING DATE: 17-JUL-90
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 07/382,518
; FILING DATE: 19-JUL-89
; ATTORNEY/AGENT INFORMATION:
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 91-1

```

TELECOMMUNICATION INFORMATION:

TELEPHONE: (916) 753-6313

TELEFAX: (916) 753-1510

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3528 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

US-08-487-087A-2

Alignment Scores:

Pred. No.:	4,226-08	Length:	3528
Score:	132.00	Matches:	42
Percent Similarity:	33.33%	Conservative:	11
Best Local Similarity:	26.42%	Mismatches:	29
Query Match:	29.66%	Indels:	77
DB:	3	Gaps:	4

US-09-854-562-2 (1-83) x US-08-487-087A-2 (1-3528)

QY 1 MetAlaArgSerIleTyPheMetAlaPheLeuValIleuA1a---ThrLeuPheValA1a 19

Db 2638 ATGGCTGCTTCATTTCTTCATGCAATTTTGGCTTGGCAATGATGCTCTTTGTACC 2697

QY 20 TYGlyValGIngly----- 24

Db 2698 TATGGTTGCTTCATTAATTTATTCCTTAATATCATCGAATAAAAAATGTAAG 2757

QY 25 LysGluIleCysCysGluLeuThrIys-ProValIys----- 37

Db 2758 AACGACATCATGTAACCGTTTAATTAACCTTAATAAATTTGTGAATTGATTACTT 2817

QY 37 ----- 37

Db 2818 GCTATACGTTTAACAATATGATAAAAAAACCCTAAATATATTATTGATTGCTCT 2877

QY 37 ----- 37

Db 2878 CTCTCATGTTATTCTAATTTTGTGTGAATGATTGTAGAGGTAGAACCTCAGCA 2937

QY 38 -----CysSerSerAspProLeuCysG1 45

Db 2938 AATTTCAGAACGACCAAGCAACTTCCAGAGATTATGTTTATGACATCATCATGTAG 2997

QY 45 nlyslLeuCysMetGluLysGluLeuTyrgLiaspGlyHisCysPheThrIleuSerly 65

Db 2998 AAAATATTGTATC---AAAGAGAAATTTACTGCGTGGACATTTGACCAACTCCAAAGGAA 3054

QY 65 sCysLeuCysMetLysArgCysAsnAlaIysThrLeuAlaThrGluLeuLeuA1a 83

Db 3055 GTGCTATGCACTAAGCCATGTGATTGACAAATCTCAAGTGAAGTAAAGCA 3109

RESULT 8

US-08-397-653B-2

Sequence 2, Application US/08397653B

Patent No. 6329570

GENERAL INFORMATION:

APPLICANT: Martineau, Belinda

TITLE OF INVENTION: COTTON MODIFICATION USING

TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSER: Calgene, Inc.

STREET: 1920 Fifth Street

CITY: Davis.

STATE: CA

COUNTRY: USA

ZIP: 95616

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0

SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/397,653B

FILING DATE: 28-FEB-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Elizabeth Lassen

REGISTRATION NUMBER: 31,845

NAME: Donna E. Scherer

REGISTRATION NUMBER: 34,719

NAME: Carl J. Schwedler

REGISTRATION NUMBER: 36,924

REFERENCE/DOCKET NUMBER: CGNE 112

TELEPHONE: (916) 753-6313

TELEFAX: (916) 753-1510

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4383 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA to mRNA

US-08-397-653B-2

Alignment Scores:

Pred. No.:	5,76-08	Length:	4383
Score:	132.00	Matches:	42
Percent Similarity:	33.33%	Conservative:	11
Best Local Similarity:	26.42%	Mismatches:	29
Query Match:	29.66%	Indels:	77
DB:	4	Gaps:	4

US-09-854-562-2 (1-83) x US-08-397-653B-2 (1-4383)

QY 1 MetAlaArgSerIleTyPheMetAlaPheLeuValIleuA1a---ThrLeuPheValA1a 19

Db 2638 ATGGCTGCTTCATTTCTTCATGCAATTTTGGCTTGGCAATGATGCTCTTTGTACC 2697

QY 20 TYGlyValGIngly----- 24

Db 2698 TATGGTTGCTTCATTAATTTATTCCTTAATATCATCGAATAAAAAATGTAAG 2757

QY 25 LysGluIleCysCysGluLeuThrIys-ProValIys----- 37

Db 2758 AACGACATCATGTAACCGTTTAATTAACCTTAATAAATTTGTGAATTGATTACTT 2817

QY 37 ----- 37

Db 2818 GCTATACGTTTAACAATATGATAAAAAAACCCTAAATATATTATTGATTGCTCT 2877

QY 37 ----- 37

Db 2878 CTCTCATGTTATTCTAATTTTGTGTGAATGATTGTAGAGGTAGAACCTCAGCA 2937

QY 38 -----CysSerSerAspProLeuCysG1 45

Db 2938 AATTTCAGAACGACCAAGCAACTTCCAGAGATTATGTTTATGACATCATCATGTAG 2997

QY 45 nlyslLeuCysMetGluLysGluLeuTyrgLiaspGlyHisCysPheThrIleuSerly 65

Db 2998 AAAATATTGTATC---AAAGAGAAATTTACTGCGTGGACATTTGACCAACTCCAAAGGAA 3054

QY 65 sCysLeuCysMetLysArgCysAsnAlaIysThrLeuAlaThrGluLeuLeuA1a 83

Db 3055 GTGCTATGCACTAAGCCATGTGATTGACAAATCTCAAGTGAAGTAAAGCA 3109

RESULT 9

US-08-397-653B-2

Patent No. 6329570

APPLICANT: Martineau, Belinda M., Houck, Catherine M.

TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS

NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/554,195

FILING DATE: 17-JUL-1990

SEQ ID NO: 4

LENGTH: 4383

5175095-4

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5	7e-08	132.00	33.33%	26.42%	4383	42	11	29	77	4

US-09-854-562-2 (1-83) x 5175095-4 (1-4383)

Qy 1 MetAlaAgSerIleTyRPhemetaAlaPheleuValleuAla---ThrlauPhevalAla 19
 Db 2638 ATGGCTGGTTCATTTCTTCATGGCATTTTGGCTTGGCAATGATGCTCTTGTATACC 2697
 Qy 20 TyRGIValGInGly----- 24
 Db 2698 TATGTTTGTCTTCAATTAATTTATTCCTTAATAATCATGCAATATAAAAAAATGTAAG 2757
 Qy 25 TyRGIValGInGly----- 37
 Db 2758 AACGACATCATGTAACCGTTTAATTAACCTTAATAAATTTGTGATGATTAATTAAT 2817
 Qy 37 ----- 37
 Db 2818 GCTATAGCTTTAACAATATGATAAAAAAACCCTTAATAATTAATTAATTAATTAAT 2877
 Qy 37 ----- 37
 Db 2878 CTCTCATGTTATCTACTATTTTGTGTGTGATGATGATGATGATGATGATGATGATGAT 2937
 Qy 38 ----- 45
 Db 2938 AATTGGCAAGACCAAGCAAACTTCCAGATTAATGTTTATGACATCATCATCATGATG 2997
 Qy 45 nlyseleuCyMetIlyArgCyAsnAlaTyRThrlauAlaThrlGInleuAla 83
 Db 2998 AAAATATGATC---AAAGAGAAATTTACTGTGACATTTGTGACAAATCTCCAAAGGA 3054
 Qy 65 sCyseuCyMetIlyArgCyAsnAlaTyRThrlauAlaThrlGInleuAla 83
 Db 3055 GTGTCTATGACACTAAGCATGTGTATTTGACAAATCTCAAGTGAAGTAAAGCA 3109

RESULT 10
 5177307-1
 Patent No. 5177307
 APPLICANT: HOUCK, CATHERINE M.; PEAR, JULIE R.; MARTINEAU,
 BELINDA M.; HATT, WILLIAM
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 MODULATIONS OF ENDOGENOUS CYTOKININ LEVELS
 NUMBER OF SEQUENCES: 6
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/554,196
 FILING DATE: 17-JUL-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 382,802
 FILING DATE: 19-JUL-1989
 APPLICATION NUMBER: 188,361
 FILING DATE: 29-APR-1988
 APPLICATION NUMBER: 168,190
 FILING DATE: 15-MAR-1988
 APPLICATION NUMBER: 54,369
 FILING DATE: 26-MAY-1987
 SEQ ID NO: 1
 LENGTH: 4383

5177307-1

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5	7e-08	132.00	33.33%	26.42%	4383	42	11	29	77	4

US-09-854-562-2 (1-83) x 5177307-1 (1-4383)

Qy 1 MetAlaAgSerIleTyRPhemetaAlaPheleuValleuAla---ThrlauPhevalAla 19
 Db 2638 ATGGCTGGTTCATTTCTTCATGGCATTTTGGCTTGGCAATGATGCTCTTGTATACC 2697
 Qy 20 TyRGIValGInGly----- 24
 Db 2698 TATGTTTGTCTTCAATTAATTTATTCCTTAATAATCATGCAATATAAAAAAATGTAAG 2757
 Qy 25 TyRGIValGInGly----- 37
 Db 2758 AACGACATCATGTAACCGTTTAATTAACCTTAATAAATTTGTGATGATTAATTAAT 2817
 Qy 37 ----- 37
 Db 2818 GCTATAGCTTTAACAATATGATAAAAAAACCCTTAATAATTAATTAATTAATTAAT 2877
 Qy 37 ----- 37
 Db 2878 CTCTCATGTTATCTACTATTTTGTGTGTGATGATGATGATGATGATGATGATGATGAT 2937
 Qy 38 ----- 45
 Db 2938 AATTGGCAAGACCAAGCAAACTTCCAGATTAATGTTTATGACATCATCATCATGATG 2997
 Qy 45 nlyseleuCyMetIlyArgCyAsnAlaTyRThrlauAlaThrlGInleuAla 83
 Db 2998 AAAATATGATC---AAAGAGAAATTTACTGTGACATTTGTGACAAATCTCCAAAGGA 3054
 Qy 65 sCyseuCyMetIlyArgCyAsnAlaTyRThrlauAlaThrlGInleuAla 83
 Db 3055 GTGTCTATGACACTAAGCATGTGTATTTGACAAATCTCAAGTGAAGTAAAGCA 3109

RESULT 11
 US-08-289-458-1
 Sequence 1, Application US/08289458
 Patent No. 5608144
 GENERAL INFORMATION:
 APPLICANT: BADEN, Catherine S., DUNSMUIR, Pamela,
 APPLICANT: LEE, Kathleen Y.
 TITLE OF INVENTION: PLANT GP2 PROMOTERS AND USES THEREOF
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: Stewart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/289,458
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Karen B.
 REGISTRATION NUMBER: 29,684
 REFERENCE/DOCKET NUMBER: 12176-4

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 594 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..270
 US-08-289-458-1

Alignment Scores:
 Pred. No.: 0.0137 Length: 594
 Score: 84.00 Matches: 25
 Percent Similarity: 44.74% Conservative: 9
 Best Local Similarity: 32.89% Mismatches: 34
 Query Match: 18.88% Indels: 8
 DB: 1 Gaps: 3

US-09-854-562-2 (1-83) x US-08-289-458-1 (1-594)

QY 4 SerTleTyRPhMeAlaPheLeuValLeuAlaThrLeuPheValAlaTyrglyValGln 23
 Db 73 ACTATTTCCTTATGATGCTGCTGCTTTTCTCTACTGATATGATGGG----- 120
 QY 24 GlyLysGluIleCysCyAlaGluLeuThrLysProValLys-----CysSerSerAsp 41
 Db 121 ---GAGGCAAAATGCTGGAGCGCTTACGCGGCAACTTCAAGGGGTGGCTTGTATGAC 177
 QY 42 ProLeuCyGlnLysLeuCyMetGlnLysGlyLysArgLysGlyLysGlyLysGlyLysGlyLys 61
 Db 178 CGGATTGTGTAATGATGTTGC---CGTAGAGAGGATTTACCATGCTGCTTGCATTTGA 234
 QY 62 IleLeuSerLysCysLeuCyMetLysArgCysAsnAlaLysThrLeu 77
 Db 235 TTCGGCTTCATGCTTCTGACAGAGCCCTGTGCTTAATTACTCTT 282

RESULT 12
 US-08-761-549-1
 Sequence 1, Application US/08761549
 Patent No. 5981727
 GENERAL INFORMATION:
 APPLICANT: BADEN, Catherine S., DUNSMUIR, Pamela,
 APPLICANT: LEE, Kathleen Y.
 TITLE OF INVENTION: PLANT GP2 PROMOTERS AND USES THEREOF
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: Stewart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/761,549
 FILING DATE: 06-DEC-1996
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/289,458
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Karen B.
 REGISTRATION NUMBER: 29,684
 REFERENCE/DOCKET NUMBER: 12176-4

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 594 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 46..270
 US-08-761-549-1

Alignment Scores:
 Pred. No.: 0.0137 Length: 594
 Score: 84.00 Matches: 25
 Percent Similarity: 44.74% Conservative: 9
 Best Local Similarity: 32.89% Mismatches: 34
 Query Match: 18.88% Indels: 8
 DB: 2 Gaps: 3

US-09-854-562-2 (1-83) x US-08-761-549-1 (1-594)

QY 4 SerTleTyRPhMeAlaPheLeuValLeuAlaThrLeuPheValAlaTyrglyValGln 23
 Db 73 ACTATTTCCTTATGATGCTGCTGCTTTTCTCTACTGATATGATGGG----- 120
 QY 24 GlyLysGluIleCysCyAlaGluLeuThrLysProValLys-----CysSerSerAsp 41
 Db 121 ---GAGGCAAAATGCTGGAGCGCTTACGCGGCAACTTCAAGGGGTGGCTTGTATGAC 177
 QY 42 ProLeuCyGlnLysLeuCyMetGlnLysGlyLysArgLysGlyLysGlyLysGlyLysGlyLys 61
 Db 178 CGGATTGTGTAATGATGTTGC---CGTAGAGAGGATTTACCATGCTGCTTGCATTTGA 234
 QY 62 IleLeuSerLysCysLeuCyMetLysArgCysAsnAlaLysThrLeu 77
 Db 235 TTCGGCTTCATGCTTCTGACAGAGCCCTGTGCTTAATTACTCTT 282

RESULT 13
 US-09-127-646-1
 Sequence 1, Application US/09127646
 Patent No. 6291744
 GENERAL INFORMATION:
 APPLICANT: BADEN, Catherine S.
 APPLICANT: DUNSMUIR, Pamela
 APPLICANT: LEE, Kathleen Y.
 TITLE OF INVENTION: Nucleic Acids Encoding Plant Group 2 Proteins and Uses
 FILE REFERENCE: 012176-004020US
 CURRENT APPLICATION NUMBER: US/09/127,646
 CURRENT FILING DATE: 1998-07-31
 EARLIER APPLICATION NUMBER: US 08/289,458
 EARLIER FILING DATE: 1994-08-12
 EARLIER APPLICATION NUMBER: US 08/761,549
 EARLIER FILING DATE: 1996-12-06
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 1
 LENGTH: 594
 TYPE: DNA
 ORGANISM: Capsicum annuum
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (46)..(273)
 OTHER INFORMATION: pepper plant group 2 (Gp2) protein cDNA
 US-09-127-646-1
 Alignment Scores:
 Pred. No.: 0.0137 Length: 594

